SUPPLEMENTALDATA

Figure S1. Sequence used for SIE-Luc, S6-SIE-Luc, and AGG-Luc constructs

Figure S2. Human TNF-α promoter sequence used for luciferase reporter (TNF-Luc) construction

(**A**) Human TNF-α promoter sequence analysis.

(**B**) Alignment between human and mouse TNF-α promoter.

Figure S3. The AGG elements of a human Alu consensus sequence

Figure S4. STAT3 mutants on AGG-Luc and SIE-Luc luciferase reporter activity

The regulation of STAT3 mutants (R382Q, R382W, R423Q, V463del, S465A) on AGG-Luc and SIE-Luc reporter was test, experiment method is same as Figure 6D.

Appendix 1. promoter of STAT3 binding sequence

Appendix 2. The sequence from chip-clone results

	HindIII-sequence (5’-3’)-SalI
Luc-SIE	ACAACAGCCTGATTTCCCCGAAATGACG
Luc-STAT6	AGCTTCTTCATCTGAAAAGAGCTTCTTCATCTGAAAAG
Luc-AGG	TTAGTCACTACTCTGCACTGAAAGGCTGTGCGCGGAGGGCGAGGGAGGGGCC
Luc-AGG- Δ 1	TTAGTCACTACTCTGCACTGAAAGGCTGTGCGC-----GCGAGGGAGGGGCC
Luc-AGG- Δ 2	TTAGTCACTACTCTGCACTGAAAGGCTGTGCGCGGAGGGCG------GGGCC

Figure S1. SIE-Luc, STAT6-SIE-Luc, and AGG-Luc constructs

A Human TNF-α promoter

(-1076) CCAGGGCTATGGAAGTCGAGTATGGGGACCCCCCCTTAACGAAGACAGGGCCATGTAGAGGGCCCCAGGGAGTGAAAGAGCCTCCAGGACCTCCAGG
TATGGAATACAGGGGACGTTTAAGAAGATATGGCCACACACTGGGGCCCTGAGAAGTGAGAGCTTCATGAAAAAAATCAGGGACCCCAGAGTTCCTTGGAAGCC
AAGACTGAAACCAGCATTATGAGTCTCCGGGTCAGAATGAAAGAAGAAGGCCTGCCCCAGTGGGGTCTGTGAATTCCCGGGGGTGATTTCACTCCCCGGGGCTG
TCCCAGGCTTGTCCCTGCTACCCCCACCCAGCCTTTCCTGAGGCCTCAAGCCTGCCACCAAGCCCCCAGCTCCTTCTCCCCGCAGGGACCCAAACACAGGCCTC
AGGACTCAACACAGCTTTTCCCTCCAACCCCGTTTTCTCTCCCTCAAGGACTCAGCTTTCTGAAGCCCCTCCCAGTTCTAGTTCTATCTTTTTCCTGCATCCTG
TCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGGCAATAGGTTTTGAGGGGCATGGGGACGGGGTTCAGCCTCCAGGGTCCTAC
ACACAAATCAGTCAGTGGCCCAGAAGACCCCCCTCGGAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTTGTGTGTCCCCAACTTTCCAA
ATCCCCGCCCCCGCGATGGAGAAGAAACCGAGACAGAAGGTGCAGGGCCCACTACCGCTTCCTCCAGATGAGCTCATGGGTTTCTCCACCAAGGAAGTTTTCCG
CTGGTTGAATGATTCTTTCCCCGCCCTCCTCTCGCCCCAGGGACATATAAAGGCAGTTGTTGGCACACCCAGCCAGCAGACGCTCCCTCAGCAAGGACAGCAGA
GGACCAGCTAAGAGGGAGAGAAGCAACTACAGACCCCCCCTGAAAACAACCCTCAGACGCCACATCCCCTGACAAGCTGCCAGGCAGGTTCTCTTCCTCTCACA
TACTGACCCACGGCTCCACCCTCTCTCCCCTGGAAAGGACACCATGAGCACTGAAAGCATGATCCGGGACGTGGAGCTGGCCGAGGAGGCGCTCCCCAAGAAGA
+1
CAGGGGGGCCCCAGGGCTCCAGGCGGTGCTTGTTCCTCAGCCTCTTCTC (+109)

The deleted sequence in Luc-TNF-Δ1： from -198 to -498 （marked with underlined）
The deleted sequence in Luc-TNF-Δ2： from -285 to -349 （marked with Italic shadow）

B lignment between human and mouse TNF-α promoter

```
Human :  TCCTTGATGCTTGTGTGTCCCCAACTTTCCAAATCCCC-GCCCCCGCGATGGAGAAGAAACCGAGACAGAAGGTGCAGGGCCCACTACCGCTT
Mouse:   TCCTTGATGCCTGGGTGTCCCCAACTTTCCAAACCCTCTGCCCCCGCGATGGAGAAGAAACCGAGACAG-AGGTGTAGGG-CCACTACCGCTT

Human :  CCTCCAGATGAGCTCATGGGTTTCTCCACCAAGGAAGTTTTCCGCTGGTTGAATGATT-CTTT-CCCCGCCCTCCTCTCGCCCCAGGGACATA
mouse:   CCTCCACATGAGATCATGGTTTTCTCCACCAAGGAAGTTTTCCGAGGGTTGAATGAGAGCTTTTCCCCGCCCTC-T-TC-CCCAAGGG-C-TA

Human :  TAAAGGCAGTTGTTGGCACACCCAGCCAGCAGACGCTCCCTCAGCAAGGACAGCAGAGGACCAGCTAAGAGGGAGAGAAGCAACTACAGA
Mouse:   TAAAGGCGGCCGTCTGCACAGCCAGCCAGCAGAAGCTCCCTCAGCGAGGACAGCAAGGGACTAGCCAGGAGGGAGAACAGAAACTCCAGA
```

Figure S2. Human TNF-α promoter sequence (GeneBank: KF887971.1) used for luciferase reporter (Luc-TNF) construction.

GGCTGGGCGTGGTGGCTCACACCTGTAATCCCAGCACTTTGGAGGCCGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCAAGACCAGCCT
GGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCGGGCGTGGTGGCGCGCGCCTGTAATCCCAGCTACTCGGGAGG
CTGAGGCTGGAGATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAG
ACTCCATCTC

Figure S3. The “AGG” elements of an human Alu consensus sequence

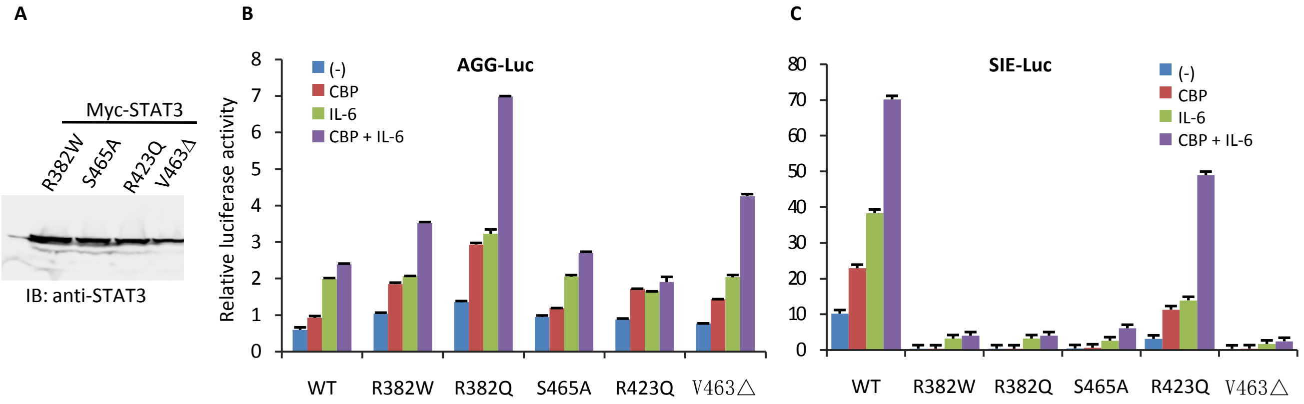

Figure S4. STAT3 mutants on Luc-AGG and Luc-SIE luciferase reporter activity analysis.

Appendix 1

promoter of STAT3 binding sequence

symbl	ref_NM	TAG_SEQ
Ptma	NM_008972	CTCCCGCTCCCCCTCCTCCCTCCCTCCCCCTCCTTCTTCCGAGCAGTCGCGAGGGAGGGGGAG
Mrpl30	NM_027098	TCCTGGGCACCGCCAGCAAATTCCAAGAGCTGACCCACTGCGCTTCCAGGAAGCGCACGCGTGAC
Mitd1	NM_026913	TCCTGGGCACCGCCAGCAAATTCCAAGAGCTGACCCACTGCGCTTCCAGGAAGCGCACGCGTGAC
BC031781	NM_145943	GCTCGCCCTTTATAGCCAGTCCCTTGAGCCCCGCCCTAGCAACCGCCCCTAGCAACGCCTAGCTCCAGCG
Eya1	NM_010164	GGAAGGGCCGGAAGGGCCTCGAACTTTCCAGTAAAAGATGTCTTCTCCTCCTCCTCCTGCTTACCCCGTAGATTAAGCACCC
Tmbim1	NM_027154	TCAGCAGCAGCGCATAAAAGCCAAGTGGAGTAGCACAGGCCTAGAGTCCCACGCTTGTTATGGAGATGTCATGCCAGGAAACGTTCAAGAACTTCAAAAA
Ddx59	NM_026500	GGGAATGCGCGGGATGCGGGCGTTGCCTGGAGCCGGAGGAGGAGGTTGTCGGCTCTGCCGC
Ddx59	NM_178052	GGGAATGCGCGGGATGCGGGCGTTGCCTGGAGCCGGAGGAGGAGGTTGTCGGCTCTGCCGC
4930523C07Rik	NM_001024470	TAGCAGAGCTGGGTGCGGTGAAACCTCAGCCAGGGACGCAGGGGGCGCTTTCCTCCACATCACACTGGTGGCACCCAC
Psen2	NM_011183	TTCCAAAACCCCTGGAAAGTCCCAGTCTTCCTCCACACTAGGGAAGGGTTTCCCCCCCAAACAGGGTACGCCCTGCGACATCTCACACA
Lefty2	NM_177099	TCTGCCCACTGTAAAAGTTTCCTAATCCACATCTGCTTCCTTCTTTGGGCCGTGGCTAATTGCCCAATCACTGTATTTCCCCA
4930511H11Rik	NM_030025	AACTACGTTTCCCAGCGTGCTCTGCTGGAAACACAATGGAGTTTGGCGTCATCCGGGTCACGTGGTCTCGCGTTT
Ctdsp1	NM_153088	CTTCAAGGGCAAGCGGGACACAGGTGAGAGGAGGGTGCTTTCTCCCAGGGCCGCAGAAGCCACCTCCG
Paqr8	NM_028829	CTGGGCAGCCCTCCCCTGGGCCGGGAAAGGGCGGAGCTGGGCGTCGCCATCCGGGTTGTCCCCTCCTCCCGGCCGCTCTC
Slc41a1	NM_173865	CTGAGTTCCCGTCACTCTGCTGCGTTTTCCCCCTCACCCCGCCCCCAGCTCAAGAAACGCCGGGGAAATGGGCGGGGCCTGGGCGGG
Fn1	NM_010233	CACGCGCGCAAAAACTTTAGCCACAACTTGAGCGGGCGCTTGAGGACCAACCCATCCCTGCCGC
Cul3	NM_016716	GTGGGCGGGGGAATTTCCGGAAGGGGGAGAGGGGAGTGTTGTGTTGTGGGCTGGCGGGGCT
Uck2	NM_030724	GACATTGCAGTTGACAGTCCTTTGTCTGCCTGCCCCCTCTCCTGAAGCACCAACACCCCTCCTTCCTAGC
Tomm40l	NM_001037170	TTTTTAAAGGGTGGGGGGCCCATCCCCCGTATGCCAGGAAAGCGAGCTCAGCTGCTCAGCAGGTA

Rrs1	NM_021511	CCCCGCGAGAAGCCGCTGCCCCGACCACGGCCGCTCACCCGCTGGCAGCAGTTCGCGCGCCTT
Adhfe1	NM_175236	CCCCGCGAGAAGCCGCTGCCCCGACCACGGCCGCTCACCCGCTGGCAGCAGTTCGCGCGCCTT
Slc9a2	NM_001033289	CCCAGCAGGGAGGAAAAGGGTTAGGCTCTGCCTGTTTCAGTAAATCTTTACAAGGAAACAGAATCTTCACAGGCAGTTCCACTTCAAAGCTGGAAAACT
Hrb	NM_010472	GAGGAAGATAGCCTGCTTACACGAAGCTCTTTGCACGTACAGGCACCCAGCGGATAAGGGCTGTAATTTATTGAC
Fbxo36	NM_025386	GGGCTCCTCCGCTGGGCCAGCCCCGCTCCCTATTGACAGCGCATCCTGTCGCCCCTCCCTCCGCAACGTTCAACTCGA
Trip12	NM_133975	GGGCTCCTCCGCTGGGCCAGCCCCGCTCCCTATTGACAGCGCATCCTGTCGCCCCTCCCTCCGCAACGTTCAACTCGA
Mybph	NM_016749	GTGGGGTATGAGGACAAGGAGAGTGTCAAAAACAAGGTAGGTTTCTCAGAAGCCACACCCCGGAACAAAGAAGGAGAGGC
2310003C23Rik	NM_029607	CGTTCCTATCCGGCAGTGTTAAAGAGCCTCCAACTTCCCCCATCCCTTACCGGAATATCTAACCCAT
Sulf2	NM_028072	CTCAGTCTCCCAGTTGGGACTGAGCGCTGGAGGAGGGTGGTATCATGTGATTTCTCTTATGT
Mybl2	NM_008652	ACTCCCAGGTTTGACTGCCCCGGGATTCTAGGAATGCTCTCCCCAGGGGTTATGTGTTGACTTGCTGATA
Cstad	NM_030137	CTCCGCCCAGCTGGGGGTGGTGTCTTCCGGGAAGTTGAGGGGTCGCACCTGGGAGGGAGGGGGAACTATCCGGTGC
Rpap1	NM_177294	GTCTTCTGCCCTTCATCCCACCACCCACCCACCCCCACTAGAGTGTTGGGAGCTACCACA
Prei4	NM_001042671	TGGCCCGACAGCCTTAGCCCATCTGGCTGGGGTCAGCTGAGGTACTGAAGGTCAAGGTGG
Prei4	NM_001042672	TGGCCCGACAGCCTTAGCCCATCTGGCTGGGGTCAGCTGAGGTACTGAAGGTCAAGGTGG
Prei4	NM_028802	TGGCCCGACAGCCTTAGCCCATCTGGCTGGGGTCAGCTGAGGTACTGAAGGTCAAGGTGG
Ndufa8	NM_026703	AAGCGTAAGCCATTCCAGGAAGTCTAGCGGTCCCGAGGGGCGGGGCTTCATCTGGTCTCCG
1700010A17Rik	NM_029309	AAGCGTAAGCCATTCCAGGAAGTCTAGCGGTCCCGAGGGGCGGGGCTTCATCTGGTCTCCG
Wfdc2	NM_026323	TGCCTTCCCCTCCCCCTCACACTAATCCACATTCCGGTAAGAGAGGGGCCAGTCAGCCAGGGAT
Mdk	NM_001012335	CCTGCAGGAGCGGGAAAATCAGCTCCGCCCCAGGCGCTGTGAGCCTAAGGCCCTAGGCAGAGGT
Mdk	NM_001012336	CCTGCAGGAGCGGGAAAATCAGCTCCGCCCCAGGCGCTGTGAGCCTAAGGCCCTAGGCAGAGGT
Mdk	NM_010784	CCTGCAGGAGCGGGAAAATCAGCTCCGCCCCAGGCGCTGTGAGCCTAAGGCCCTAGGCAGAGGT
Ada	NM_007398	CCCCCCCCCCGCCTGCAACTCTGGCGCGCATTTCCCGGAATTCTGAACCCCAGACCTTCCCTGCTGGCTACACCCTAGGAAGCTCC

3300002I08Rik	NM_027017	GGCACACGGAACATGCCAAGCAGAAATACTCAGGATTGCCCTGCTTCACAGAAAGGGCCATACAGAAACC
Cpne1	NM_170588	CAACACCTCCACAGCCGCTTCACAAAATGGCCGCCCGCCCGCTCCGGCGCTCCGCGTTCCCGGAGTAGGCGGGGCGCCGCTGCCGACGTCA
Cpne1	NM_170590	CAACACCTCCACAGCCGCTTCACAAAATGGCCGCCCGCCCGCTCCGGCGCTCCGCGTTCCCGGAGTAGGCGGGGCGCCGCTGCCGACGTCA
Rbm12	NM_170598	CAACACCTCCACAGCCGCTTCACAAAATGGCCGCCCGCCCGCTCCGGCGCTCCGCGTTCCCGGAGTAGGCGGGGCGCCGCTGCCGACGTCA
Rbm12	NM_029397	CAACACCTCCACAGCCGCTTCACAAAATGGCCGCCCGCCCGCTCCGGCGCTCCGCGTTCCCGGAGTAGGCGGGGCGCCGCTGCCGACGTCA
Rif1	NM_175238	AAATCTCAATGGAAGGAATGTGGGTGGTGGTGGGGTAAAGGACGGAAAGATTCCACGGATTTCCCCACT
Cstf3	NM_145529	TGTTTCAGGGGGTAGTTCTGATCACCTGGCAACCGCACCTTTGTTTCAGGGGTTAGTTCTGATCACCTGGCAACCGCACCTTTGTTTCAGA
Cstf3	NM_177253	TGTTTCAGGGGGTAGTTCTGATCACCTGGCAACCGCACCTTTGTTTCAGGGGTTAGTTCTGATCACCTGGCAACCGCACCTTTGTTTCAGA
Cstf3	NM_001037326	TGTTTCAGGGGGTAGTTCTGATCACCTGGCAACCGCACCTTTGTTTCAGGGGTTAGTTCTGATCACCTGGCAACCGCACCTTTGTTTCAGA
Asxl1	NM_001039939	GAATCAAAAAAAAAGCTTTGAACGGGTTAACCGCGCGCGCGGCCAGGGGGGAGTCCAGCCACCGCCCCTTCCCAGCACCACCTCCCAGAAACCCTCAGGCCTCCGCTAGTTCCCGAACCTCGCGAGACCCCGCCCCA
Endog	NM_007931	AACCAAAACCAGAAAAATACAGTTTGCAGTAACAAGTGCCAACCAGAAGGTGGCGCTCTCACACATGACAACTCA
Adal	NM_029475	CGGCGTGCGCCGCACGGGTCCCGGGACCAGCAGCGCCGCAAAGGGGTCGCGCACGTATCCGTGTGCGG
Slc27a2	NM_011978	GCGGTGCGTTTATAAGGTACTTGATTAAGCAAAGGCACTGCGCTGTGTGATAAGAATAACTAACC
Rab14	NM_026697	CGCAGCCAGCGGAGCCCGGAAGAGGGTGGTGGAGACTAACCTGACGGCCACGCCCCTTCGTCAGTTCGCCCCTCCGGAGTAGACCCGCCTCGGCCTCGGCCCGCCCCCACTG
Rbm18	NM_026434	GCTTCGGGTACTCACCTGCTAGCCTCAGAGCTGTGCCCTCAGCTCATGCCCCGAAAGCAGCTTCCGACGCTGGGGT
Mrrf	NM_026422	GCTTCGGGTACTCACCTGCTAGCCTCAGAGCTGTGCCCTCAGCTCATGCCCCGAAAGCAGCTTCCGACGCTGGGGT
Orc4l	NM_011958	CAGCGCCTTGGAGCCTTCTGGGAAAACCATCTCATTTCCTCCCCTCCCCCTCCTCCTTGCCTTCCACCAACCAGCCTCCCGTCAGAACGGGACATGCGCAGTGAGTGCCTCCCGTCTCGTCTCCCCGAG
Rif1	NM_175238	ACCTGTGTATCCCAGGGCCACCGTCACCCCTCTACACCTGGGGTCCAATGGAAGTAAACCAATTC

Pak6	NM_001033254	CCTCTCATTTCCTCTGTGTTTTTTGCTGAGTCACCTTATCTCCCAGAGCTGCAGTTGGCTGTTGGCATCTTTTGGAGGAGGGGTGGGGCTTCCTGGAATTC
LOC433479	NM_001013802	ATTTTAGTTACAAATTAACATTTAGACCTATTGGCTATAAAGGGCTAAGGGGCCACAGCAGT
Nxt1	NM_019761	CAACATCCAATCAGAGCTCCCTCAACCGGATCTTCTAGGATAGTGCCTAACCCGGAACCTACACTGTCTTTGCCGCCACA
Stx16	NM_172675	CCGCTCCCGGAACGTTGCAAGCAATCTCATGAATGTCGCAGGGGGGCACCCGCGAGGAACGG
Tmem79	NM_024246	CATTGACTGACGTCCTCCAAACCAGGTTCATGTCCTTCATTTGCCCCTCTCGCTATGTGACCTT
Tpd52	NM_001025263	GCTGAGCACTGGGAAGCGGGCAGGGGAGGAGGCCATGCACATTCACAAACAAGCATCAGGAGTTG
Tpd52	NM_001025264	GCTGAGCACTGGGAAGCGGGCAGGGGAGGAGGCCATGCACATTCACAAACAAGCATCAGGAGTTG
Tpd52	NM_009412	GCTGAGCACTGGGAAGCGGGCAGGGGAGGAGGCCATGCACATTCACAAACAAGCATCAGGAGTTG
Sox2	NM_011443	ATGCCAGGAAGTTGCGTGACCCTCCCCCCATCCCCTGCACTCGGGAGCTTCTTTCCGTTGATG
Ccna2	NM_009828	TGATCTGGGATTAAAGGCGTGTCTCTATGCCCCGCATTCCAGTAAACTACCCCACCCCCACCCCCAATTAAAGATGGGTTA
Mcl1	NM_008562	GCCCCTTTCCCCTTTTACGGGAAGTCCTCGCCTGCGTCAGCACGGCCCTAAGGCGGCGGCAGGGA
2700083E18Rik	NM_001029890	CCTCTGAGATCCCGGAACTGGGGGGCTGGGGGAGGGGGAAGGGCTTGCTACCTCCGAGAAGAGAGGGAACCACATCCTCTACCGGGGGTCCCACCCCCAACC GAACGCCCCTTCCTGGCCCC
Sox2	NM_011443	AACAGAGCTTTCCCCCAATACTGGTGGTCGTCAAACTCTGCTAATTAGCAATGCTGAGAAATTCCAGTTAACAAGGGCATTCTCC
Wdr77	NM_027432	GCAAGATGGCCGCTCGCACATCTCGCGAGAAGAGATCAGCTCGCTTTTTCTCGGAAGTTCTC
Dnttip2	NM_153806	CTAGTCCGATGGCGGAGACCGCTGGCCAGAACTGCAGTGGAGCCGGGGAAGGAACGATTCTCC
2310010I16Rik	NM_025519	CGAGCCCGGCCAGGAAATGCCCAAGAGTGGGTGTCACCTGCCGAAACAACTTGTTGATTCCCAGGAGCTCTGTCGGCTCCGACTGTGGCTTACCTGTCTC
Tiparp	NM_178892	GACACTCCCCTCCCTCCTCCTCCTCCTCCCCGGAGCGCCGAGCCGCCGCGCGCCCCTCCGTCC
Scamp3	NM_011886	CTGGGCTGCGGAGACTGGCTTAGGGATATCACGTGCGGTACTTCCCGCTTTTGGGTTTTTTTTTCCT
Dennd4b	NM_201407	ACTTCCCGTCATTCGGCATGTGGGCGTTGGGACCCAAAGTGGCTCCAGTGCCGTTGTTTTCCCCCAAGGGAGAA
Adh7	NM_009626	CGTTCTGCTGTTTTTCCCTACTTAGGCTTTCATCTTACATCCTTTGTGCTAGCCCTTGTTCCCAGCCTCTCCCTGTTCCGAAAAGCATCACCTTCCATC
Cyp7b1	NM_007825	ATGCTTAATGCAAACCTGAATAGCTACAGCCTGCGTGGTGCAACTCCATTCGGGCCTCTCAACTGTAGCCCGTGTGTGAGTGTGTGGAGGGTGAAAGAAGTCTTT ATTAGGACATCCACTGGCT

Pcdh18	NM_130448	AAACCCTATAGACAAACTCAGAAAACTACCATAAGCAACTGGGACTTTAGAAACTCACAGCCATCTGGCCTATG
Kpna4	NM_008467	TCGTTCTTTTCTCCCCCGGTGTTACTTGAGCGCTTCATTCACTTTGGAAGGCAAAGAGGT
Hcn3	NM_008227	GCGCACCCACCGCTTCTCTAACTCTGGAAGGCGCAGGGGAAGCGGCTCACTGGCCCGAAGGGCC
Clk2	NM_007712	GCGCACCCACCGCTTCTCTAACTCTGGAAGGCGCAGGGGAAGCGGCTCACTGGCCCGAAGGGCC
Csf1	NM_007778	GCATTGTTCAAAGAATCTACTATACTACTATACTATCCTCTCCCCTGGCTGTAGGGAGAAGTGGGGAGCATCCAGCTACCTGGGTAGGAGAGGAAGGACTTGGTCC
Ddah1	NM_026993	GGATTATTTAAACTTTGATATGTGAAAGAGGAAAAAGAACAGGCTTTGTATCACCATCAAAGAAAG
Rpl22	NM_009079	TTCGCAGTGGGACAGCCCGTCTGACTCCTCCCTTTCCCGACAGCCGACTTCGCCCTGGGA
2410081M15Rik	NM_028603	GCTAGGGCTCTGGAGACTTCCCAGAACTGTTGGGGGAGCCTGGAAACTGTTGCTGGGGAGCCTGGA
Fabp3	NM_010174	GTGGGACTGCGGAGAAAGGCGCAGGCGGGAGACATTCCGCAGGGAGGGGCTAGCACGTGT
Spsb1	NM_029035	GCTCCTCACAGCCCTCCCCTCCGCACTTTCCCGCTTAGCCCCGCCCTACACCACGCCCCTTCTC
Sdhb	NM_023374	CCCTTTAATGAGGCTACCTGGCAGAGAAGCCAGATTCAGGGTGAGTTCCCAGAAACTTGGCCC
Scp2	NM_011327	GCGTCGGGGGCGGGGCCGCAGCGTCAGGGGCGGGGCCGAGTTACGGGAACCGACCGGAGGAGGCAGG
D630039A03Rik	NM_178727	TGGCTGTCCTGGAAAGGTCAGCCTCAGTGGGTGGAGGAGGGTCACAGGCTTGAAGAGGAAGCC
Lin28	NM_145833	ACTGCTCTGGTCTCTGACACCTCTGGGGTGTCCCTTCCCAGAACCTTGAGATTTGACACCCCCT
Hes5	NM_010419	CCCCACCCCGCAGTGCTTCTGCCGGGCAAAGCCCGCCAGCCAGAGGCAGCCTTTACCCCTCCCCCTT
Orc3l	NM_015824	GAGGCATGGCGTGTGGCTTTCGTAGGTCGATCGCCTGTCAGGTACAGTCCAGAGCGGCGAGCCAGCGGGAGCCAGGGCC
Rarsl	NM_181406	GAGGCATGGCGTGTGGCTTTCGTAGGTCGATCGCCTGTCAGGTACAGTCCAGAGCGGCGAGCCAGCGGGAGCCAGGGCC
Nipsnap3a	NM_025623	GGGGTTCGTGGTGCGCGTGATGACGACGCTGCGAGGTGGGCGGGTCTGCAGTGCGGAGAACGGGCCGTATTCTGGGAACTGGGCGGAGC
Cpne3	NM_027769	TATCGCCGCAGAAGTCGAGTGAGGGTGGAGAGCCAGCGAGGAGCACCGCAAGGCGGCAGGACCGCAGGGGCTTTAC
Dnajc6	NM_198412	GAGTTACAACCCAGTCCACCAGGTCGATCAACCCAGGCGTCTTTCACTTCCAACAAAGACCAGCT
Prdx1	NM_011034	AGTGCTGGAGCTCTACTCGCATTCTTCACGTGGCGCTTAGTTCCCGGACCTGTTGGAACCCTGAGGCTAAC

Psmb2	NM_011970	GCTGTCTCACTGGTGAGGTCGTGTACCCGGGAAGTGTCCCTGTCCGTGGCCTCTGCAGCCTCCCGCTTCCCGGCACCATGGAGTAC
C79267	NM_183148	CCCAGTGGTCAGCCGAGATTTCTCATCTGTCACGTGGTCCTAGCGCTGGCTCCTCTGGAATGCTGAGAGGCCACATCTGGCTGTGACGAGGCTG
Aco1	NM_007386	GGAGGGCGCACCCGGACTAGACTGCAAGCTTCAGCCATCGCTTGCAGCTTCTAGAGGGAGGA
Tal1	NM_011527	TTCCTGGAAACTCGCTTTGGGCGCGGCAGACCGCGCAGGACCTCACGGCAAGCTAAGTAACTGCTGGTCTCTCAGCG
Hnrpr	NM_028871	CTCTCTCTTATTGGCCCGTCAAGCTGCCCGTCATACGGTCTCGTGGGCCGATTGGTCGGCCGCACGGAGTCCCTGGAAG
Ankrd6	NM_001012450	GCAGAGATGTCCTAAGCAGTGGGTGAGGGGCTTTCCTGCAGGGCTGGTGTCCGGGCGTGAATAGCATTTGGTAACCC
Ankrd6	NM_080471	GCAGAGATGTCCTAAGCAGTGGGTGAGGGGCTTTCCTGCAGGGCTGGTGTCCGGGCGTGAATAGCATTTGGTAACCC
2610528J11Rik	NM_025572	GTGAGTCCTCCCTGCTGAGGACGCTGCAAATCCTGGCTGGTGCCCCGCCTTCCCTTCACCTGCACTTCCGCCCCGCCCACCT
Smap1l	NM_133716	CAGACAGATCCCTGGAAGGCAAGGTTCTGGTTGTGCTCAGCCATTAGTCAACAATGGGCACAGGCAGGAAAACAAAGCAATGCTGAGTTACTTGGTTTCTCTGCTTGTTTTTCCTGCTGCCAGAGGCATTTCCTTCCTGTGCTGACA
Tcea3	NM_011542	GCTATAGCCAAGGACTTTTCAGCTCCTCCCCCGGCCACCTCCTCACCTCCCCACCCCCTGCTGACATGTCAGTGATCCCCAAGCTTTGT
Agtrap	NM_009642	TAACAGGAAGTCTCCCCTGCTGAGCCTTCAGACATGCTGAGAGCTCTCAGGAGGCGGGAGCTGCCCAGCCTGGGCTGGTGGGTGTGACT
Epha7	NM_010141	CAGTAGCTAAAAGCCAAGTGCTCCCGACTGCACGCCGCTGGCCTAACGCGGCTCGTCCCCGCTTTCCCGGCAACCGATCTGGGAGGGAATCCTGGAC
Topors	NM_134097	AGAACCCATTCCTAAATTGAGCGTTCACGCCCTGCCCTCGGCTCCGCCTCTTCCTGGAGGACACGCTTTTCCGCCTCTGACGTC
LOC622404	NM_001037913	AACAGTGACTTGCGGGGGAAGTCTACGCGCGTGTGCACGCGGCACTCTCTGCCCGTGGTCCGGGGACTTTCCCCTAGGCGAAAGGATAAGGAACATGTC
Akap2	NM_001035532	TTGGCTGGTTTAAACAAGACATCATTTAATGATGTCAAGCCCAGACTCCTGCGACCCAGATTCCTTAGCCCTTTCCCCTTAACCCGCTGGAGTTTCTGGTGGCTTTGATTTTA
Akap2	NM_001035533	TTGGCTGGTTTAAACAAGACATCATTTAATGATGTCAAGCCCAGACTCCTGCGACCCAGATTCCTTAGCCCTTTCCCCTTAACCCGCTGGAGTTTCTGGTGGCTTTGATTTTA
Akap2	NM_009649	TTGGCTGGTTTAAACAAGACATCATTTAATGATGTCAAGCCCAGACTCCTGCGACCCAGATTCCTTAGCCCTTTCCCCTTAACCCGCTGGAGTTTCTGGTGGCTTTGATTTTA

St3gal3	NM_009176	CACAGCATCCCAGTGTCGGCCCGTCAGCTGAGGACGGACAGCTGCTGCCAAGCACCCACAATAGGCTTGTCTTTTCCCGGCAGAATGCATCGAGGGTGGAGTGAGAAGGTGAAAGGTCGGACACGTCATTCCTTTTCTGTGTACAGCTT
Zmpste24	NM_172700	CACCTGAAATATCCCTCCGGATTCTGTGTGCAGGGATCCAATTCAAAGGTTCCGGCCTTCTTCCTGGGAACGTCAGTGTGGTCGCCGCCTCTCCTTTGCTTTGGCGGGTTACCAGAGAGGGCAATGGACCCCGGTGCTTAA
Gjb3	NM_008126	AGGAGGCATCTCTGTTCCAATATCCCCTTAGGGTCTGTTCTCAAATTACTTCGAGTCTGAACCCGCCC
Phactr4	NM_175306	ATCCTACCTGGTCTCTGGCCGCCTGGCTCCAGCCAGAGCCTTCGGCCCCAGGGGAGGGGG
Necap2	NM_025383	CACTCTCCTCCATCTCTATCGCCCGAGCCCTCGGGACTTCCGGCTTCTCCCCGCCCCTTCAGGACCGGAAGTGATGCGACTCTATGACCAAGTTCTGTCTAGAGCGGAAGCT
Tmem142a	NM_175423	CCACAGGAGCAGCTGCAAAGAGAAGCGAGGCCTGACAGCGTGGGGCGCTTCCAGGAAGGCGAGC
Wsb2	NM_021539	CTCCTCTCCCCTTAGTTCCTCCCCCTTGGCTTTCCCAGCATCCCTCCCGCTGGGGCCGTTG
Noc4l	NM_153570	TCCCGGTTCCTGGAAACCGAAGTGTGCGCCGAGCGGAGTCGCGCCCGTGACGTCACCCGAGCC
Ddx51	NM_027156	TCCCGGTTCCTGGAAACCGAAGTGTGCGCCGAGCGGAGTCGCGCCCGTGACGTCACCCGAGCC
Ephb4	NM_010144	GGCTACTGCCCCAACATGCACAATCAGGGGTAGTAGGCATGGGACACCCAGCACCCCTGGACAGTCCCTAAGT
Fastk	NM_023229	AGGCGCTGCGAGCAGAGGAGCCGCGAGCCCCGCCCTCCGCTTCCGGGAAATGCGCACGTCGCGGGGGCGGGG
Crot	NM_023733	CCTAGGCTGCAGACCCCGGGAACGCAGCAGAAAGTCAGATAAGCGCCCTGCAGTCCCCGCTACA
Tnip2	NM_139064	CGTCCTGTCTACCAGACCTTGGGTCCCCAGACGACATGGCTGTAGGCCTTCCGTGGGGACTTGGGCGTCTCCAACTTCTCCACACAGGGGGAGCGAAAACCAGCCTT
Msx1	NM_010835	CAGCCTCTCTTGGGCCCTTTCAAAAACCAAACTGCACTGAAGTACTAATGGTGCCGCTGCCA
Apbb2	NM_009686	GGAAACGCTTCCTTGCCTGCTCCCGCCTCTGCGTCCCAGCCCGGTCGCCTGCTTCCTAGGCTCATTCCCTTGGCGGCCTGC
D430033A06Rik	NM_177007	TTTTTTTTTTTTTTTTTTTTTTCCCGGAAGAGACGAAGGAATGCTCAGTGCGCATGCGCGGTCGTTCGCGGCCTT
Cd38	NM_007646	CGGCGGGGGGGAATCTTCCAGATTGTCCCAAACAAAGAATCTTGTGTTGTGGATCAGCTGGAAGC
Gtpbp6	NM_145147	CCTTCCTTTCTCGTGACTCCGCCCCTTCCAGAACTAGGCGTCACCGCCGCCCCAATTCCCCGTGGCCTTCCTGTATAGCACTAGTAAGT
Cit	NM_007708	AGAGAAAACCATACCTGATGCAAACTGCAAGAGGTTTTATTGTTAGCTAGCTGAGGATGAACTCC

Serpine1	NM_008871	TTCCCTTGACTGGAACATCCCTGTGCCTTTGGCTGGTCGGTCGTCTAGACCCTTGGAAGTACCACAAGA
Brca2	NM_009765	GATGGGCGAGCACATGCTAGCCGGGAACAGGCACAGAAGGAGCTGCTCGCTGACTTCCCGGTGGCACT
BC057022	NM_001004180	GGGAAGCAGCTGGCAGCCGATCCGGTTTCCAGGTAAATCCCCGCCCCCACCCACACTCCGGGAGC
Ubc	NM_019639	CACCCAGATCCGTCCTTTGCAGGTGACCAGGGACTACCGCTTCCGAGCCGGCACCAATGGGGACCGAGAAAGGGCCCCAGCAACAGAGAGGGATTGGCTGAGGCCGCCTACG
Dhrs8	NM_053262	GAGCCACACCTTAAAGGACCAGGAAACAAGGAAGGGGACTCTTTGGGGAAAGGAAGAGAAGTAGCAAGAGGGGGATGGGAGG
Golga3	NM_008146	CAATAATACAAACAAGACTGACAAACACTTAGGAACAAGTTGTCAGAACTGTGGTGGAGGCGGT
Coro1c	NM_011779	CACCACCTGCATGCAGTGCCCTCATAGGTCAGACCAGACTGAGCTAGCCTGAATCTGGAGTGTCCGCAGGCT
Fbxw8	NM_172721	GGGACGGACTGTCCATCCGCCGGAAGTGTCCGTAGTCGGCCTGGAGACTTCCGGGAGCGCGTCTTGTAGGTTCCGG
Anapc7	NM_019805	GGCGATCAGAGATCCAGCTCATCCCTGTAACTATCTTTTCTTCGCACTTGGATCTAGCGGGTCACTTGGACGGGCAAGCCATGCCT
Rabl5	NM_026073	TGCAGTTAGCAGGACCAGCTTTGCCTTTTCTCTTTTGGTCCTCCTCAGCTTCCATCGTAGGCCACTTTTCCAGGCTCCCGGAACTGTCAGGGTT
Mospd3	NM_030037	TTCCGGGTCTTCCCGCTCCGATCTCCTGACGGACTCTGCTCTTTGAGAGTCCCTGACCTCCAGGTCACCGAATTGTGTCCCTGTGCCCTTTCCTTGAGCTCGGCATATGCTCTGCTCGGGATCC
A930017N06Rik	NM_175522	AGGGATGACTTGGATCCCCGGAAAGCACACATTAACTCCCCCCCCCCACACACACAGAGGCTAGT
Cyp51	NM_020010	GTAGGATGTAGTCTCCGGAATAGCTTGGCCGATTCCCAGCAGGTAGCAGCAGGGACAGTGGCTGAACAATAGAGTG
Serpine1	NM_008871	CATCTTGCCCTTCCTCTTTGTGTGTCTCTAGTTCTCCCCCTGAGACGTCTTGCTCACTGCCCCT
4933411G11Rik	NM_177880	CCCCAAGAATTGCACAGAAACTCTGTGTCCCAGACGCCTTCGCGCGCCACTGCATCTAGGGATCCTCGCGCAAGAACTTACCTCCTCCCAGCAGTTTGGG
Rbak	NM_001045482	CCCCAAGAATTGCACAGAAACTCTGTGTCCCAGACGCCTTCGCGCGCCACTGCATCTAGGGATCCTCGCGCAAGAACTTACCTCCTCCCAGCAGTTTGGG
Rbak	NM_021326	CCCCAAGAATTGCACAGAAACTCTGTGTCCCAGACGCCTTCGCGCGCCACTGCATCTAGGGATCCTCGCGCAAGAACTTACCTCCTCCCAGCAGTTTGGG
Fbxl13	NM_177076	CCAGGAAAAAGCTGCTTGCACTAGGGGCATCCCGCCTGCCTGGTGAAAGGAACCGCAGCACACAGGGTGGGAGGGCTTCCGATTTTAG
2810037C14Rik	NM_026034	CCAGGAAAAAGCTGCTTGCACTAGGGGCATCCCGCCTGCCTGGTGAAAGGAACCGCAGCACACAGGGTGGGAGGGCTTCCGATTTTAG

0610009O03Rik	NM_026660	AGGGAACCTCCCTGGATAGCAGCCACACCCCGGAGGCTTCGGAACAGGCACCTCCTCTTCCGGGAGGCCGTGCTGTGGCGGGAACTGGGTTTGGAGTCTCCCA
D5Ertd585e	NM_027922	TGAGAGGGTAATTACAGGAATGTGGGTGCAGGTGGAAAGCCTCCACACTGCAGCACAGACAGAGCACTCCTTCCCTTGTTTCCCCTCTCTCTATACTCTA
Rfc5	NM_028128	CGGTCTCTCATGATTCCTTGGGTGTGCACCGAATTGGGAATTGAGTGGGGGGTTTCCCCACTAGGTTCTTTCA
Ppp1cc	NM_013636	CAGAGCCGGAAGGAGCTGGTGAGCCTCGCAGCGCGCAGCAGACTGACAAAGTCCACCTTCAACTTGCGCGCGCCAA
P2rx4	NM_011026	CTCGCCGGGCTCTAGCCAAGCCACCTGGAACCAGCTTGAACAGGACACTGGGGACTACTGGACGTCCTGGGAGCTAAG
4930438O03Rik	NM_029112	GCACACTGTGGGAGGAGAGAGCTGACTCCTGCGTGTTGTGTCTGACCTCCACATAGCGAGCAC
Cldn4	NM_009903	TTAAAGCTCCTAGAGGAGGGGCGGAGGCAGAGGGAGGGGTTTCAGTCCCGGAGGCCTCCCTCGGGA
Ars2	NM_031405	AAAGAATGACGGGAAGAGGGTGGAGACGCGGAAGTCTCGCGTGGTTTTGCGACAAAATCGCCCCAGCTTCTCGGAGCTACGGAAGTTGAGCTGGGCCAAGCC AGGCCTTCTGAACGTGC
Bcdin3	NM_144913	GGGGGGGGGGCGCGGAACTAAAGATGTCAGCGAGGATTATGGAACTTGTAGTTTCACTAGGCTTT
Zcwpw1	NM_001005426	GGGGGGGGGGCGCGGAACTAAAGATGTCAGCGAGGATTATGGAACTTGTAGTTTCACTAGGCTTT
Gpr146	NM_030258	CCAGCATTAAGGCGGCCGGCCGTGGCTGGCCAAGGGGATTGTCCGTTCGGACTGGGGGCGGAGCCTGCGGGAACTAAGCACCGGTTCCAAGAAA
Uspl1	NM_001013378	TCGCCGCAGTTCCCACTGCGCCTGCGCCTGCTGGGCGGGCAAGCCACGCCTCTGCGGAGCCCTGCCGGAAGTGCTCTGGTCTT
Skap2	NM_018773	ACCACGCCCACACACAGCCGGGAAGGCCACGCCCATACGCGGAAGCGAGCAGGAGGCGAGGC
C1rl	NM_181344	CTATTCCTGAGTCTGTCAGCAGGTGGCAGACCTGCACCCAGAGTCTCAACTCATTTCCAGTAA
C87436	NM_146170	TGCGCAGGATGCCGGGAAGCGGGTCGCATGGGAAGTGCGTTTTCCAGCCGGCCGTTCCCGGAAGC
Trh	NM_009426	GGGGACCCGCCCGCTTTCCGGAAACCTGGTGGGGGCCGAGCGAGCGAGGAGGCGCGGCTGG
Ube1c	NM_011666	TAGCACTCACCTCAAGGTCTCAGAGTTGAGTATTTCCTGCACTGTAGGCCCTTAGAAGACAGAGCAAGGCAAGCATTT
Arl6ip5	NM_022992	TAGCACTCACCTCAAGGTCTCAGAGTTGAGTATTTCCTGCACTGTAGGCCCTTAGAAGACAGAGCAAGGCAAGCATTT
Tmem40	NM_144805	CCTCAGCCTGCCTCAGCCTGCCTCAGCCTGTTTCAGCCTGCCTCTGCCTGCCTCAGCCTGCC
Nanog	NM_028016	AGCCAGTTCTCTGGACTCCTCCCAGCTCTTACAATTCCTCTCCCGGACGGTTCCTAGAAGACAAAGGCAAGC
Grcc10	NM_013535	CTAGGAAACCAGAGAAGGATCAAAGCCCCTCTCACACACCGGGGAGCGGGGAAGAGAACTGTTTTGCT

Ldhb	NM_008492	AGAGATGGTGAGGCTTGGCCAAGGTCAGAACTTCCCATGCAGCTGCGAGGCTTTTCTCTGTGATGCA
Gm1070	NM_001033462	GAGCCGCAGAGCGGCGGAGCAGCTGGGAACCTGGGATTGTTCTGGAGCTCGCCGGAACTCACCGGAACTCGCCGCCCTGTG
A2m	NM_175628	TAATCCTTCTGGGAATTCCGGCTAACGGGTCAGGAATTAACCTTGGCAGTAACTAGGCCATCAATGACCCCTTC
Pdk4	NM_013743	CGGGATGACGTGGGCCCCCTTGGGATAGATCCCAGGTCGCTAGGACTTCAGGCCCGCCCAGACT
Cbx3	NM_007624	CCTGTTCCAGTAAAGCTCGTGGAGCGCCGCCACCCCGCCCCCACCCCGCGCCTCGGTGGCTTCAGAAAGCAA
8430410A17Rik	NM_173737	GGCTTCCTGACCCTTAGGGGTTTGTGGGAATAGCTAGAGAGTCTCAATTCGGATGGCCTTACACATTGAGGGTGGGCAGCACAGGTTTTCTGGCTTCAGATTCCGGCCTGGGAAGGG
Krcc1	NM_145568	CCTCCAATGGCAAGAAGGACCGACACCCAAGCTCCTACCCACACGGACAGAGCCGGTTAGTCCGAAATGGCGGGAAG
Prmt8	NM_201371	TTTCTCTCTTTCGGGCCATCTGTCAGGCATTGAGGGATAGAACAATGGGGGAGGGAGGCCATACTCAGGAC
Tulp3	NM_011657	GGTAAACTCCAGGGGAGCGGCTCAAGAGTGCTGGCGGCACGGGATGCACAGCGCATTGCAAATG
Ergic2	NM_026168	CGCGATACTTTCCGCGTTGACGGTATGTGATCTAATCAAGCGGCGCGGTCAACCTGAAAGGGGCGTGGCTACGTGGAAACTAAGTGAA
Ergic2	NM_026355	CGCGATACTTTCCGCGTTGACGGTATGTGATCTAATCAAGCGGCGCGGTCAACCTGAAAGGGGCGTGGCTACGTGGAAACTAAGTGAA
Ezh2	NM_007971	CTTGCTGGGTGGAAGCACCACAGTCGCTGTCTTTGTTCTTTTGCCAACGTGCGGTACCTCTCAGGAAAGCCATGGACAGGCAGGCGGAGG
Adipor2	NM_197985	GGACGAGGGCGTGCTGAAAACACTGGGCTAAAAGACGCCCTAGCCGTCCTAGGCCGTTCAC
Ncapd2	NM_146171	GGGGCGTGGCCCCGAGTCTGCGCTTTCCCGGCATCTCTACCGTAGTCGGCTAAGCATGGTCACCCGTTGTCTCTCCGCGGGCCGCCTAAAGCAGTC
Mrpl51	NM_025595	GGGGCGTGGCCCCGAGTCTGCGCTTTCCCGGCATCTCTACCGTAGTCGGCTAAGCATGGTCACCCGTTGTCTCTCCGCGGGCCGCCTAAAGCAGTC
Asns	NM_012055	GCGTGCGGGAAGTTTCATCATGTGGCTGGGACCCAACCCGTGCGCAGGGGCGTGGCCCGCAGTG
Hirip5	NM_020045	GAGAGCTGATGATTGGGCAGATAAAAGGGAAGGTGGAATGGAAGGTGGAGAAAGAAGAAGGAGAAAATGGATGAAGGAGAGGACGCGGAGGAGG
Clec12a	NM_177686	GCACGCCAAATTGGGAATTGAGTGGGGGGTTCCTCACTAGGTTCTTTCACAGCAAGGACGGTCTCTCATGAGTTCTTGGGGGGTCTCGTCATCCTGAGACTTGAATGA
Etv6	NM_007961	TGCTGCGCCCGGGTCGCCGCGCCGCGACCCGCACACCCCACGCCGTGCTCGCCGGCTCCTACGCCCC

Cmas	NM_009908	GGTTCTCCCAGACGCTTTCAGTACTTGTTAGGACTCCTCCTGACTGGCATACTCCACCCCCTACCCTA
Kras	NM_021284	CGCGAGGGTGGTGCCGAGAGGGCGTCGGCCAACGCGGACCCCGACCCGGGGCTGGCGCTCCCGATAGCCCCGCCTCGCCGCTCGT
ZBTB45	NM_001024699	CATTGGCTTTCCATTCCTGCAAGCTCCAGCTAGGAAGGTTTCCCCACTTACTGGAATGTG
Sema4b	NM_013659	AGCTCAGCCACTGACAAGCCCAGAACTGGTTGTTTCAGGAACCGCCCAGAAAGCTGCTGTCCTTTTCTGGAAGATAGCA
Trim6	NM_001013616	TACCTGCCCCGACCCGGTCTACACCGGCTGCAACCAGTCGGAGCTAGGAGCCCTAGGGCCTCTCCAGAG
Bbc3	NM_133234	CCCTAGGTCTGGGCTGTCCCCACGCTGCTCCTCCTGCCTGGACCAGGCCTCGCCCCGCCCCTC
Aldh16a1	NM_145954	AGGCTTCCGCACTGTAGGGGAAATCACGCGCTCAGAGGGGCGGGGCTTCCGAGAAGGCCGCAGTGGATGACGGGAGCCCGC
Nop17	NM_029406	AGGCTTCCGCACTGTAGGGGAAATCACGCGCTCAGAGGGGCGGGGCTTCCGAGAAGGCCGCAGTGGATGACGGGAGCCCGC
AI428936	NM_153577	CCAGGTTCTTCCAGGAAGGGGTGGAGCTAGGCTGGCCCCTGGGCCCCTCAGTAGCCTCGGAC
Fah	NM_010176	CCACCCCCCCCCATCTCCATCCCGGAACTGTCAGACCGTTCCGCCCCTATGTCTAAACCTCCCC
Nup98	NM_022979	AAGAGGAGGAGCGTAAGGAATTGCCGGGAAAGGGGGGGGGGGGGGGAAAGGAGGGACGATGGGGAGGGATGTAGAGTCCCACTCCCTCTGCCGCAACGGTTGGCTGAGAGA
Arl6ip1	NM_019419	CGCCCCGCAGTCTGCTTATATAGGCTAGCTGCCTTTCCCGACAGCCCTCGCGAAACTCGCTCCTCATTGGG
Hsd3b7	NM_001040684	GGGGTGGAGGCTAGGCTGGTCTCCTTCCTGGAATGGGTCAGGAGGGAGGAGCGAGCGGAAGGAAGGA
Hsd3b7	NM_133943	GGGGTGGAGGCTAGGCTGGTCTCCTTCCTGGAATGGGTCAGGAGGGAGGAGCGAGCGGAAGGAAGGA
Cic	NM_027882	GGCAGCAGCCAATAGGCTTAAGCGCAGGGGGCAGTGCTTGCGCGGAAGGCCGCGGGGGAAGCGGGGAAGG
Zfp36	NM_011756	GAGGGGGGGCTTCCTGGAAGCCGTGACGAGGACGCTCAGCCCGGACGCTTGGGTTCCTTCTC
Fchsd2	NM_199012	CCCCAGCGGGCTGGCGGGAAGGCGCGCGGGAAGCCCCCAGCTGCCTGCTCGGTGTGGGGGGAGGGAGGACG
Sbk1	NM_145587	ACCCGGGTGGCTTTGCACAGCTGCTGCTTCAGCCAGGAACCCCCCACCCCCTTCTTCCGTTCTGCTATACACCTTTA
Leng1	NM_027203	CCCAGGACTACAGCCTCCAACACCTGTCAGCTCAGACCCTAGGCTACTCCTCAGACTCACCTTCTTCAGGCAGAACAGT
6330581L23Rik	NM_146185	CTCCCAGGAGAGGGAAATACAACGCCTGGAAATGTCAGGGGCTGAAAGCTGTGGCCTGAACAACAGATACAA

Ppme1	NM_028292	AGCAAAGCATCATGGGTGTTGTAGTCCATTTGCAGGGGCTCTAATTGGCGCCTTCTTTTGGCACCGCTTTCCGGGAACTGTTG
AU020772	NM_001017985	AGCAAAGCATCATGGGTGTTGTAGTCCATTTGCAGGGGCTCTAATTGGCGCCTTCTTTTGGCACCGCTTTCCGGGAACTGTTG
Relb	NM_009046	TCGGCCGGGAAGCGAAGGCTTGGCACTTCGCAGGGTCCGGGTGCGAGTCGCTGCCCATTGCCT
Ccne1	NM_007633	GGTTTCTGCACAGGCCTGGGGCCCAAGCGGAGCCAATGACATTCCTCAGGAGTTGCTAGGCTGACTGGAAGTGGGCTT
2310044H10Rik	NM_197991	CCCATTTTTGTATTTTTGAGACAATCTCAAGCAATCCAAGCTAGCCTCAAACTCCTTGATCCTCCAGCCTCAGCCTCCCAAGCACGGAGATGAGAGGCTAGCTACCACTACTCCACGCAGCTCAGGTTCCGAGCAAA
Btbd1	NM_146193	GCACCCGGCGCGCCGCCGCCATGGTCGAGCCGCCCCGAGGCCGGCACCGCCCCCCTGCCT
Mesdc1	NM_030705	GCCACACCCACTCCCTTTCTTTGTGCAGACCTTGTCTGCCAGAAACTCCTGGAACACCTGGGCCTCCTCCCAGTAA
Nupr1	NM_019738	CTACTTATAACGCTGTCTCCTCCCTAAACCACGGGGTTGGCCCCCGCCCTCCAAGCCCTGTCTGATGCAATCTGGCCCTTTCCCA
Zfp629	NM_177226	CTTAACCCCTTAAGTGCCCTGCCTCGGGGGACGGGCTAGATGCCGGGAACTCTAGGGTCCTTCTCAAGGGGTGATTCCAGGCTGAGGACCCGGGGACCAGTTCAGGGTGACTGGGACGGAGCAGGAAGT
B4galnt4	NM_177897	CCAGGAAGCAGTCAGTGTTCCTTCCATGGTCTCTGTTTCAGTTCCTGCTTCTAGATGCCTGCTTGAGTGCACGCCCTGGCTTT
Nipa2	NM_023647	TCGGACAGCCTTCGGCCGCACCGCGGCCAGCACCAGAAGAGCCGCCGAGAACCTGCCGGGAAACCTG
A230056P14Rik	NM_001033396	TCGGACAGCCTTCGGCCGCACCGCGGCCAGCACCAGAAGAGCCGCCGAGAACCTGCCGGGAAACCTG
Pwwp2	NM_001033206	AGAAGCAGAGTGGGGGAAGGGCCTGGACCCGGGGAGTGTCCCCGCTACCCCTCGGTTCCTGGCAAGGCCTCCTAGGGGGCATTCCAAGCCTGCGTGGCGT
Chmp2a	NM_026885	CCTGCTGCGGCCGCCGTTTCCGGATTAAGCGACCTGACGTCACACGACCCACCCTCTCCGGGAATGCTGGG
Npas1	NM_008718	GTGCCTGTCTTCGCCCCGCCTACAGCGGCCCCTGCCTGCTGGATAGTTCCCATTCCGGGAACTATCTGGGATAGTGTTGGCCTGGTGTGTCTGA
Bcl3	NM_033601	TGGAAGGCCCTGTGCCTGGGGACCCAGCAGGGATGGAGGGGAGGGGAAGGGAGGCAGGCCTGGAAT
Erf	NM_010155	GGAGGATGATCAAGAGCACAGCCATTTCCCAGCCTGAGTTTACCCAACCCCCTCAACCCCGAGCCTGAAAGAGGGCAGCTGTCCAGGGGTGGGGTGGAATGGGTGGGAAACATTTCCCA
Zfp36	NM_011756	GCAAGCACTTCCGGCCTAGGGGGAGGTGAACTCTGAGCTGAGTTTCCAGAAAAACAAGCAGGGACGGGAAACGCGGGGGTGTGAGAGCCAGTG
Herc2	NM_010418	TCGAGAACCTCGTCCCGCTGCAAATACCTTACCAACTTCGGGTCCCTGGAAGCAAACACA

Zfp446	NM_175558	GCAGTGGGACGTGCTCGGTGTCACTTCCTGGAAGTGCCCCAACCTCCTGGGGCTCTCCCACGCGTCAGAGGTGAGCTCACTCC
Mark4	NM_172279	ACCTCAGGGAGGGCTGAGACTGCAGGTGTGAGCACCACACCCAGTTGTCTCTGGTTCTGGGAATTGTTTGT
Apoe	NM_009696	GAGACAAAGTCCTCTGCCAGCTCTCGGGGCCAGACTGCACAGAGGCGAGTGACCTGGAGCCACCCTCCTGGTGAGGCCAGGCCTCTGATGTTC
Bcl3	NM_033601	CTCGGGGCTTTCCCGGACATCCCGGGAGGTGGAGCACACACTGGGGTTGAGTCCAGGTCACTGAGTCACAGGGAGGCGGAGGGGGGCGGGGCGGCTTTGTAGACTTAGAGAGGCAGGGGAATAGCACCGCATGGC
Samd4b	NM_175021	GCGCTGGGGTGAACTGACTGGAAAGGGGCCGGCTCTCCAGAAGGGTGACAGCAACGTGGCTTG
Gmfg	NM_022024	GCGCTGGGGTGAACTGACTGGAAAGGGGCCGGCTCTCCAGAAGGGTGACAGCAACGTGGCTTG
Gmfg	NM_001039192	GCGCTGGGGTGAACTGACTGGAAAGGGGCCGGCTCTCCAGAAGGGTGACAGCAACGTGGCTTG
Nfkbib	NM_010908	AATTCCCCAACACGCCCCCTCATATACCCAATCAAAATGTTTTAAATAGCTACACCCCGCCCCTGTACTGCACCACA
Sirt2	NM_022432	AATTCCCCAACACGCCCCCTCATATACCCAATCAAAATGTTTTAAATAGCTACACCCCGCCCCTGTACTGCACCACA
Capns1	NM_009795	CTTCACGCACAATAAACTAGACTGCAAGGCTGACTTCGTCTCTCTTAGCTTGCCAGAGTCTCTGCCCTCTTACTCCCCCTAC
Chchd8	NM_183270	CTGAAGGCGGGCTCTACACGGAGAGTTCACCAATGGGAATTGCAGAGGGCTCTGTTCTTCCGCGTGTGTGCTCCCGCTGGGTC
Art1	NM_009710	GAGTCTGCCTGGTTCCTGTGCTTTCCTGGCACTGCTATTCCGTATGCAGGCAATGTGCAGCCAGTGTCTGATCCTTGCCCTGGTCCCCAACCCTCTTAG
Cyb5r2	NM_177216	CTTCCTGCCCCGCGCTTTCCCGGCAGAACTCACCTGGAGCGAGATGCCTGACTTATCCTCGAGATGAACAGTGCCTTTGATGGTGGGGATGATGAAACATCCGGCAGTG
Cttn	NM_007803	CCCGCTCACCGCACCAGCAGGGTCCACCAGGCTCCCGCCGCGCCCCGCCGCTCCCTGTGCCC
Ccnd1	NM_007631	CTCAGTGCTGTTACTAGGCGGACCGGGCAGATCTCCACGAGGAACTTCGTTGAGCTCTGCGCTC
Nol3	NM_030152	GAGTTCGCAGAGCCAGTGAAGCATGCCCTTCCCCCACGCCATTCCCAGCAGCCCTGGCCGC
Rbm35b	NM_176838	CCTCCCATTCCGGAGCGCGCCTGCGTCAGTCCAGGCTTTCCGGTAAGGACACTCCCTTCCAAC
Lsm4	NM_015816	AAGCTGCGTTTCCGGGAAATGGGCGGGCTTAATGGCTCACGTGGGCTTCGTTGCCCTCTTG
Hook2	NM_133255	CTCCCCTAAACCGGCTCAACCGGTGGACGCACCCTTTTCCCAGAAGGATGCGTTCCTACGTTCTGCGCGCCC
1700041G16Rik	NM_175196	GCCACAAAGAAGATCTTGTGCCGGTAAACACTCAGGAGGTAGTGGTGAGGGGTGGGGATGACCG

Unc13a	NM_001029873	CCGTAAATGACGGCGGCCAGGAAGCTCAGGGGCCGCACAGGAAGGAGCAGGGACTTTCCTGTCG
Jak3	NM_010589	CCGTAAATGACGGCGGCCAGGAAGCTCAGGGGCCGCACAGGAAGGAGCAGGGACTTTCCTGTCG
Card15	NM_145857	GTCCCCAAGGGCAGAACACAAAGCACTGCAGGCAGGCCTGTTCCCGGATACCTGTCTCACCAGTCC
BC057552	NM_172502	GGCCGGCCGGTTGGGTGACAGCCGGCATTCCTTGTCGCTTCCCGCTACGCTTGTCCATCAAAGCTATCTTGGTTTTTGGTTG
Hook2	NM_133255	CCTTAGGGAGGGGTTGAGTCACTCACTTCCCAGCAGTACAACTCAGGCTGGGTCCAGCTGTTCCTGGAAACATGTTCGAGGTGG
Galns	NM_016722	GGAGTGGGCTGGGCCTTACGGGAAAGGGGCGGGACCAAGGCCGGACCTGAGAGTCTGGGCGGA
Trappc2l	NM_021502	GGAGTGGGCTGGGCCTTACGGGAAAGGGGCGGGACCAAGGCCGGACCTGAGAGTCTGGGCGGA
Large	NM_010687	CCGGAGCCCGGGCCGGGTCTCGGGAAAAGGGTGCTAGCTGGAGCTCCCCGCCCTTCTTTCCCGGACTCCGGCTACCCCAGA
Hook2	NM_133255	GAGCTGGGGAAGGCCCCGTTCGTTCGGCCCTGGGGCCCCAGTTTCGGGTCGGGCAGGAAGGG
Katnb1	NM_028805	CGGATTTTTTAAACACAACCGGGTTCCAGGAAATGCAGGAAAAGGGCGGAAAAAACCAAGCCT
Thap1	NM_199042	AGTGTGGAGGGCCAGAAGGATGGTGCAGTCCTGCTCCGCCTACGGCTGCAAGAACCGCTACGACAA
Aars	NM_146217	TTGAGCATTGCATCAGCCGAGCCCAGGAGCCTTCCCAGAAACCGGCTTGTTAGCTCATTCGCG
Trappc5	NM_025701	CCAATTCCATTTCACAAGAGTGTTCTTGCTTCACCCAGAGAGGCGTCCTAGGCTCCAGTTCA
Slc25a4	NM_007450	CCTCCTTTGCAGAGGGCATTGGGGGCGAAGACGCTTCCGGGAGCTAGGGGTGGGTTGGGGGCTGTGCCTGCAGCTTGGGACGTTTAAAGGG
Kifc3	NM_010631	GGGGGATGGGGGAGAACTACTCGGGGGACACAGAGGGAGGGCCCAAACAGTAGCCTTCCTGGAAGCGACCCTT
Tssk6	NM_032004	GCCACCAGCGGAAGTGAGGCAACGCGCGACCACCATTTTGAGTGTGGCGGAAGTTCCGTCACCCAGGAGGTTCCCTATAATTTGGAAGCG
Rbmxrt	NM_009033	TTTAAAAAGACTGGGCAAGCAGGCCAGGTGACACGCCCCTTTAATCCCATGCCTGGAGGCAGAGGCAGGTAGATCTCTTAGTTGCAGGCCAG
Asf1b	NM_024184	CGCTGCTCTCTGTGAGGTGCGTCTACCGGAAAAGCGGAACGAGGGGCGGGGGATGCCGGTGCGGTAACCCTTGGGATTGGACAAGAG
Mt3	NM_013603	ACCCTGAGACCTGCCCCTGTCCTACTGGTGAGCCCCTTCCCCCTCCTGCAGCACTTTGCCCTTTCC
Sntb2	NM_009229	GCTTTCAGTGAACCAGGACAACCTCGCCTCCCGGAAGCGGCCTCGCCGGCCTTCCCCCCGCCCCTCCGGAAAGTGGGCGTGGCCCTCATGA
Aprt	NM_009698	CGTTCCTTCCCTCGCGCATAGTACAAGGGGCCTGAGATTCAGCCCCTGCTTTCCTGGAATTAGCCCGGAAGGGA
Dlc1	NM_015802	ACCGCACACCAGGCCCCGCCCAAAGCTCGCCCAGGTCCCGCCCCACGCCTCCTTCCCCCTTTCCTGG

Ssbp4	NM_133772	CGCGCAGCCCTTGCTCGCCTTGCCGTACATGCTCCGCACCTGTCAGGCGCGCGTGGCCATCGCTGCCC
Ssbp4	NM_133772	CCAGGGCTCAGCTGGGCCGACGCCGGCCTTTCCCATTTCCTGCTTGGCCCGCCACCCCCTC
Mtap1s	NM_173013	CCAAAGCCTAGCGGGCATTGACAGAGGGGTGGAGAGGAGGGGGCGCTTCCGGCCGGGGTCTCCGGTG
Elmod2	NM_178736	AGGAGGGATACCGGGAACTCCAGCCCTGGGATTCGCAGACACACCCTCTCTGCGCCCGGGCCCGAGGAGCTGTCAAATTCGAAATCCCCG
Dpep3	NM_027960	GTGCCTGAAAGTGCTGGTGCCTTCAGTGGGGTCAAATATTCTGTGATGTGCTAAGTTCTGTGTAGAGGAGTG
Nfat5	NM_133957	TTGATGCTGTTCCGTGGCGCGCCTGTCCGCCCTCCGCCGGCCGCCAGGCTCTTCCGGGCTCCCGGACCTCCCCCCCTCCGC
Nfat5	NM_018823	TTGATGCTGTTCCGTGGCGCGCCTGTCCGCCCTCCGCCGGCCGCCAGGCTCTTCCGGGCTCCCGGACCTCCCCCCCTCCGC
Clcn3	NM_173876	AGGTTGCATTCTCCCATACCAACAAGGCAGGGCAAGTAAGCAGCTCACTGCAGCACGGAGGACAACAGCCAGCCTGTTCCCA
Armc6	NM_133972	GCTCCTCACCGGGTCTACGCAGCCACGTGGGGAAAGGGTGGGGCTCGCAGCTGTCACCCGAGACTT
Sfrs14	NM_172755	GCTCCTCACCGGGTCTACGCAGCCACGTGGGGAAAGGGTGGGGCTCGCAGCTGTCACCCGAGACTT
Nr2f6	NM_010150	CAATCTCAGCAGGTGCCCTACTGCTGAGCAACCACCAGCCCTCTACTTCCTGTAAATGCTGGTTCTAAAGCAGCCTGGGGT
Ier2	NM_010499	ATTCAAATAACCCCTTTCATTTGCTGTGCAGGCCCTTTAAGAAACACCCCCTGCCAGCGGGCAGACTTCCCGCCACTGCAGCCGGCCGACTTCCC
Junb	NM_008416	ATACTGAATTTGTCAGCTGCGGAAGTGCACTCCGATTGGCCGACGCGGGAGCCAGGCCCCCGCGGCCCCCTCCTAGAGCGTGGGGAAGGGGAGGAGGCGGCTCGCGTCACTGTCAGGAAGCGCGTGTCCTTG
Mt1	NM_013602	CTTCTGGTGTGTCTGAAGTCAGCTACAGTGTACTTAAAATAATAAATCTTAGCCGGGCGTGGTGGCGCACACCTTTAA
Mt1	NM_013602	AGCCAGTCGTGCCAAAGGGGCGGTCCCGCTGTGCACACTGGCGCTCCAGGGAGCTCTGCACTCCGC
Gfod2	NM_027469	ATCCAAAGCACCGATACCGGGAACACGCCGCCTGGTTTCTAAGGAACAGGGGTCTCTGGTAC
Vps4a	NM_126165	GCCCTTTACCGGTATCCCACCAGACCCCGCCCCCGGCAGGCCCCGCCCCTCTTAGAGGAGCGGTGTCTGCAGTTGCAGGCCATGGCCAC
Sf3b3	NM_133953	GAATCGCTTCAAGGCCTAAGCCACCGCCACTGCCGATCCGCCGGCGTCCGCCATTAGCCTTCAAGACGGGCCTTCGGGTGCCGCGCGAC
Cog4	NM_133973	GAATCGCTTCAAGGCCTAAGCCACCGCCACTGCCGATCCGCCGGCGTCCGCCATTAGCCTTCAAGACGGGCCTTCGGGTGCCGCGCGAC
1700030J22Rik	NM_027103	CAAGTCGCGGCCCCCAAGAGCCGGGCTGTTGCCCTAGGTTACGGCCGCGTCGGAGGCGGGCCTAGGTGCAGGCATGCCGGAAGTGACGTAACCCC

BC019943	NM_144927	CTCTAATCTACACAAGAACCAGAAGTGGAGGATCCTCCTAAGTTCATGTCAGACGGGTAATGTGCCCACGTCGTAACAAGGTTTATGGGCGGCAC
Gsr	NM_010344	ACGCGCTGCGGGGCGGGGACAGGGGCCCTCGGGCGCGGTGCTTAGTCACGGCGACGCTGCACCC
Zfp42	NM_009556	AGAATCCCGATCGCCTGGCCTTGAGACTCAGTCACATCTCAGTACCTCTGTTACAGACTTGTAACCGAATTTACACAAG
Hmgb2	NM_008252	CCTCTCTAGACCGGTTCCAACGGGTCTGGGAGTTAACGACCTGGGAGACCCACCGAACCTGCTAGGCTTAGCCTGGAGGGACGGGC
Arrdc2	NM_027560	GGCTCGTATTCACTCCTGAGCCCAGCTGTGTGAACGAACACAGGTTCACAGCCTTATGAACCAGGCTGCAG
Gcsh	NM_026572	CGCAGGCTGTAGGCCACAACCCGCAAGCTCCTCGACACTTGCAGCGACATGGTCAGAGGTCCGGAGGGTAACTGCGCTTCGCCTCCGCCACCGGGCCGGT
Taf1c	NM_021441	GTCTCTATAGCCACGTGGTCTGCCACGTGCTCTCAGCATTCCCGCAACAGCCTCACCTGACCCCG
Itgb1	NM_010578	GAGTTCAGGGCAGATCTCTGTCACCTGACTATTTCCCAGAATTGCCCCTCCCCCTGCCTCTGCCTCTCTGCCTCACTGCC
Tdgf1	NM_011562	TGGTGGGGGGGGGGAATCTGCTATTTCCGAGAAGGCTGGGCCTCCTTCATTAACAAGCTAATGG
Lrrc2	NM_028838	TGGTGGGGGGGGGGAATCTGCTATTTCCGAGAAGGCTGGGCCTCCTTCATTAACAAGCTAATGG
Lrrc2	NM_028838	GAGGGACATCAGGGATTTTCCTGGAAGAAAGCTTTGCTGGGCGTTCATGTGACTCATGTTC
Icam1	NM_010493	GCCCTCGTTCCGGAGGGGAAGGCGCGAGGTTTCCCGGAAAGTGGCCCCGACAGCACCGCCCCT
Tdgf1	NM_011562	AGGACCCTCAGGTGGGCGGGGAGACGGGGCCCCACGCCCATTACGGGGCCCCACGCCCAT
Cmtm6	NM_026036	GAGGGCGGAGTTGACCGGAAGCGTGGGCGGAGTCCCAGGAAGTGACGCCCCCTACCGCTCG
Loh11cr2a	NM_172767	GTCTTCCTGGAAGTTCTGCTTTAGTTACTTTCACTTTTAAAGCTGCGGAGACTTTAGGAGGT
Tmem24	NM_027909	GGGTGGAGTGGGGGAGGGTTGAGTTGCACACGTAGAGGATTCCGGGATGAGAATAGGCGGAGTCT
Gtf2a2	NM_001039519	TTCCCGAGCGCCAGCAGGAGAGACCACGCCCCTTCTCGGAAACGGCGGTGGGGGCCGGCAGTGGCTCCTGTGGCGTCACC
Vill	NM_011700	TGTTGCCCACAGGCTGAGTGAAGGAAGGTGCAGAGGCAGTTCCCAGAAGGTAGGCCTGGACTGGGGTGGGGGTGGGGGACCCGGTAGAGGGGTTGC
Pkm2	NM_011099	GTGGTAAGGATGTGGCCATCAGTGGGGGAGGAGCTTCCTTCTGCCTTTAATTCTATCTGGG
Smad6	NM_008542	GCACCACGCCCCTTTCCGGGCAGGAGCGGGGCCCCGAGCTCAATGAAAGAAATTCCGCTACTCTCATTGGCCTGG
Plekhq1	NM_153119	AATGGACGGAAGAACCTAGGCGGAGCTGAAGTAGCAGGAAGAGGGCGGAGAGAGGTTTCCCGGACCAAAGCAGGGAGAAGGACTGGGAGGGGGTAGAG

Plscr1	NM_011636	CCATTTCATTCCACCGGAAACACCTCTCATCAGGCCTTCACCTTGAGTGCCTCCTTTCTCATGCTTTAG
Stag1	NM_009282	GCGCCTCAGCTCCCTCCCCTTTCCGGGCAGGCCCGTCCTGTCAGCGGAGCAGTGAGCAGCGCGGCCAGCAGAGGGCGGTCGGG
Cish	NM_009895	GTCTCACGTCCAGCGATACGATTGGTCAACTCTAGGAGCTCCCGCCCAGTTTTCCTGGAAAGTTCTTGGAAATCTGTCAAAGGTGTTTCCTTTCTCG
Trim71	NM_001042503	GTTATTGGGACTGATCGGAATTCGGAATCCTTTTAATCTCCAAAGGAGCAAACTCACTTCC
Arhgef12	NM_027144	GGCGCGACTGGAGCGCGCCGAGCCGTCCCCTCCCCCGCCGACTTTTTTGGGCCCTTCTCCCTGGGACTTCGGGAAGCCGCTTCACCC
Scap	NM_001001144	CGCGCCGCTCGTGCCCGGGAGTTCCGGGATGCGGGCGAGCCCGGGCAGGGGCGCGCGGGCGTGGGCGC
9530077C05Rik	NM_026739	GTCCGCGTTGTGCACGCTGGGAGTTGTAGTTCGCTTCCCTTCTCTCCCTACGAGCAGGGTGTCAGTCGCAGGAGCGCCTCCAGCGGCGAGCATGTTTGGTGGCGTGGAGTGCGG
Bcl9l	NM_030256	GAGCCTCTAGGGCTCAAGACTCCTCCCCTTCCCTCCCCCACCTTCTACCGGGATCTCTGCTGGGGGCGGGGAAAGGGGACAGAGCAGGGGGCGGTTGCTTGAGGTGTCT
Suhw4	NM_146224	GGCGCATATGGCCGCGCTCGCCTCCCGCGTTGGCGGGAAGACTGGGAGCGCGGACGCGCGAGGC
Parp16	NM_177460	CCGGGGCGGGTCCCGGGGCGGTTTCCACTTGGGGCGGTGGCGAGGATGACTAGCAGCCGCATTGGGCA
Ttk	NM_009445	AGAAGCGTTTCTCCTAAGAGCAGCTGAGCTCATAACTGAGACAGCATCACGGGGATGGGGGCGGGGGGGGGGAA
2610101N10Rik	NM_026476	CTCCGCGGCGCCGGGGCCGCGTGACTTCCGCGTCGAGGCGCTTTTACGCGCCCCGCCCACCCCG
Slc25a36	NM_138756	CTTCTCCAGTAAGGCTTTACCGCCGAACCTCTCCAAACAGTGCCGCCAACTGAGGACCGAAGTATCACATGCCGGAACTATGGGGGGCATTCTCATT
Icam1	NM_010493	TCACTGCGAAAAGCAAGAGCAGTGGAGCACGAGGCAGGATCGGGAGTTCAAGGTCATCCTCAACTACAGGGCGTTTGAGGT
Spbc24	NM_026282	GTTTCTAGCTGTGCAACTTGTGCCAGTGACCTTGGCACAAGATCTGGCAGGTTCCTACCAGATC
Hspa8	NM_031165	GACCGAGGGTCGTGTGGGGGAGGGGCGCAACAACCTTCGCAGCCATTTTGTCCTCGCCCCACTTCCGTCTT
Gclc	NM_010295	CCCCGCGGGGAACGCGGCAGCCTCTGCTCGGGACCGGACCCCCGTGGGCGGCCAGCCCGCGC
Parp3	NM_145619	CTCCTAAGAAACAAGTTCCAAGTCTGGGATCCCATCTAGCGACCCTTCGTGAGCCTTCAGCTAGTTTTT
Rnu3ip2	NM_145620	CTCCTAAGAAACAAGTTCCAAGTCTGGGATCCCATCTAGCGACCCTTCGTGAGCCTTCAGCTAGTTTTT

Ube1l	NM_023738	CTTCCCTCTCACACCGCGTGCCTCGTGCTGAAGACAATCCAACCACTTGCCAGGAAATGGGAGGAGCCTGAGG
Dalrd3	NM_026378	TGGCGACGGCGCAGCGCTCCATGAGAGGCGTGGCCGAGCATGGATTGGCTTCCCGGCAGCGCGAGGGGGTGTGG
4733401H18Rik	NM_023247	TGGCGACGGCGCAGCGCTCCATGAGAGGCGTGGCCGAGCATGGATTGGCTTCCCGGCAGCGCGAGGGGGTGTGG
Myd88	NM_010851	TCCAGTACGCTCGCCTGTGGAGTTTCCTACTTCCCTTAAGTCTCCTGCCAGCCCCTCCTTCTTTCGCTTTCCGAGAAGCTCCGCCCTTTGCTAGAATCTAGACTACGGGGCCAGAACTACCCAGCCTA
Acaa1a	NM_130864	TCCAGTACGCTCGCCTGTGGAGTTTCCTACTTCCCTTAAGTCTCCTGCCAGCCCCTCCTTCTTTCGCTTTCCGAGAAGCTCCGCCCTTTGCTAGAATCTAGACTACGGGGCCAGAACTACCCAGCCTA
Sec63	NM_153055	AGGTTTGGCAACCTCGCTTAGGTTGCAAAAGCTCAGGTCCCAATCGCACCTAGGACGCTCGCCTCTGCTC
Socs2	NM_007706	GCCGAGTGTGCGCGCGACTTCCCAGCCCGACGCGCCTCCCTCGCTCCCCGCCTCCCGCCCCTCGCGCC
Tbc1d15	NM_025706	CGGTCGGGCTAAAATAACATCCGGGCGGGAAAGGGGCGGGGAGGAGCGGGAACAGCAGTTAGGCGCATGCGT
Dnmt3l	NM_019448	CCTCAGAACTCTCTCCCTCCCCCACCCTTTCCCCGAAGCCCTCTCCCACTCTCAAGGCTT
Cd63	NM_007653	CCGGCTCCTGGCTCGAGCCTTCCAGGCAGCGGCCACGTGGCCTTGTCCTGGCGGGGGGCT
Cdc2l6	NM_198164	GTGCTTCCCGCTTTTCTAGCCTAATGACAGTCAGGGCCGGGTATCTACTTCCTAGCTCAGCAAAGGTG
Crsp3	NM_027347	CAGCGCTGTCAGCTTACGGGGTCACCTCTACGAGCGGAACCAACAGGCTGAGATACAGATTTCAGAGGGGCTGG
Suhw2	NM_177475	AGAGAGAGAGAGAGAGAGAGAGAAGAGCCTTTGGGGTGGGGGAAGGGAAGGGCAGCCCAGCCCCTGGGC
Ikzf4	NM_011772	GGGTGAGCCCAGCCACTCACCTTCCAGGAAGCGTGGATTCCTGGAAGTGAGGGGAACCGCCGTCATTTCGCAGGCAGTGGCAGCCGCACGGTGAGCAGGGGCCCACGGCTGCAGCCGG
Tfam	NM_009360	CTCTCTTGAGGGTAAAGGGGACTTCCAGCTCGTCCTTTCAAACCTCCTGTCACAACAGCAACAAGA
Ptges3	NM_019766	AGCGGAGCGAGGCCGCGCCGGGAGCCCCGGCTGCCGGGAAACGGCCCCTCGCCCTCCCCCCACCCTCGGCCCTTCGCCTTTCTC
Pdss2	NM_027772	GGGGTGCCAAAGGGCGGACACCGACGTCCTGGGGCACAGGCTCCCTTCCATCTCTCGCCTTCCGG
Midn	NM_021565	TTCCCGTTCCGCCCCCCCCTTCCACACGCGGGCGCCCCCAGGCGGAAGCACCAGGCCAACAGGAAAGGGGGCGGAGCAGGGAAGCAGGCCAAACACCCCCCCAATCCTAATGTGAGGT

Syn3	NM_013722	CTCCCTAAGGCCAGAAAACCCACCTACTCCACTTTGCCTTGGCTTACCGACAGTGCCAGCTACGGTGGCCCGTGTGTACCTCGGACTGGCGCCGCCAATTACAGGATCTGCGGGAGCGCTG
Helb	NM_080446	TTTCCAAGGCTCTGCTACACAGTTTGAATTACTACCAGTAACCAACTGGAGACAATTGTCTTACTTAGTTG
Mbc2	NM_011843	AGGGTTGGATGGCGGGAAAAGGGGGGGAAAGAAACCAAAAGACAGTATTTGACTGGTCACGGAGAGAACGGGGCGTAGCGTC
Ndufs7	NM_029272	GGAACTCTTTGGAGGACGGACCGCAGAGGTTGTCTGAAGGCCGAGGCCAAGATGGCGGCGCTGGCGGGTG
Ap3d1	NM_007460	GGTGGAGCTTGAGCAGAGGACCTCAAAGCCCGCCCCCAGAGTGACACACTTCCTACCAGGTCACGCCTAGTCCAGCAGGGCCACACCTCCCAACAGTGCCACTTCCCATGGGCCA
Mgat4c	NM_026243	ATTATTTCTCAGGACAGTTTCTAAGAGCCCCTAACAATAGCATATTTGCATACTGGGTTCCAGCAATGGTCAGGGTGGGTCAGGGTGACTTTCTTTGAATGAACACTCCTTTAACCCAGGAAGCAGGTGGGTGGAGGAATGTCACTGTTTTATGAT
Stat3	NM_011486	GGGGGGAGGGAGGAGACATTAGCGGAATGTCCTGCTGAAAACTCAGCTGAGTTCCTGGCAGT
Stat3	NM_213659	GGGGGGAGGGAGGAGACATTAGCGGAATGTCCTGCTGAAAACTCAGCTGAGTTCCTGGCAGT
Stat3	NM_213660	GGGGGGAGGGAGGAGACATTAGCGGAATGTCCTGCTGAAAACTCAGCTGAGTTCCTGGCAGT
Socs3	NM_007707	TGTAATGTTTAGTCACTACTCTGCACTGAAAGGCTGTGCGCGGAGGGCGAGGGAGGGGCC
6030413G23Rik	NM_178664	CGATGCACAGACTGGACCGCTTCCGATTGGTGCAGAGCCACGTGGCTCGCTAGGGACTTACGGGTATGGGAGGGCTGTTAGGGGAACAG
Hoxb13	NM_008267	AGACTCTTAACTTTCAACTTGGCCTTGACCTTCCTGGAAGTGTCTGGCGGGTATGTAAAGG
Cnp1	NM_009923	GTTGTGGGAAGATCTGATACAGTGTGACAGTACCATTGTGGGAGGGTCTGATACAGTGTGACAGTACCAGAGCAGT
Arhgap27	NM_133715	ATGCCATCCACATACATGAGAATACAACTACACACCATCCACATACATGAGAATACAACTACGTGCCATCCACATAGATGAGAATAC
Cobl	NM_172496	GATATGACCCTGGACCTTCCTGGACATCCTATATCTACTAGAATAAACCTAGACCAGATACAGGGT
Tha1	NM_027919	CTCTGCCTGATTCCCGAATTCCAGTCCTTAGAAAACAAACCCTTATCTCATTGTCTGGCTCCAGGCTTCTGCTGGG
Mllt6	NM_139311	CAGGTCAAGGACAAGTTCTCCCCCTCCTTGCTTCCCCCCTCCTGGGCGGGGACTCATCTCC
Nf2	NM_010898	AGTATACTCCTACTCTAGCAAGACTGGTTGAGAAGGAGCGGGCGGCGCCTTTCCCGGGAAACCTGTAGAG
Upp1	NM_009477	GTTTAATTGGATTTGAAAGGGCCAGTCTTTTCCGGGACTGGAGAGCAGGGAATTTCTTGTCTCTTGAGTTGGTAAA

Upp1	NM_009477	TCTGTCCTTGGGTGACCTTAGCCGAGAGTGAGAGCAGCTTCCCGCAATAAACCAGCATTGAATGTTATCTA
Rtn4	NM_194052	GCCGGGAAGGTGAGTCACGCCAAACTGGGCGGAGAGTCTGCCCTCCTCTCTCAGTTGCTCA
Rtn4	NM_194053	GCCGGGAAGGTGAGTCACGCCAAACTGGGCGGAGAGTCTGCCCTCCTCTCTCAGTTGCTCA
Rtn4	NM_194054	GCCGGGAAGGTGAGTCACGCCAAACTGGGCGGAGAGTCTGCCCTCCTCTCTCAGTTGCTCA
Rtn4	NM_194051	GCCGGGAAGGTGAGTCACGCCAAACTGGGCGGAGAGTCTGCCCTCCTCTCTCAGTTGCTCA
Psmd3	NM_009439	TCCTAGAAGATCCGCCTTCATCGTGCACCTCGGCTGTTGATTTATTTTCCCTCCCTGGAC
Map3k14	NM_016896	GGCTGCATTCTTTTTGAGGTTACGGGAAGGAAGGGCGACTGTACGCATGCGTGGGCATTCCCGGC
Vdac1	NM_011694	CTCCCTGTACGCCCCTGTGACTCAGCAGCTTTCCCTGCCTGGCTTTAACTCCGGGAATGGGCTGGGTGTTTGTTGCCGGGTAGATAGAGCTGCAGACT
Pipox	NM_008952	TTTGTCTCAGGACTTTGCCCGGAATTTCAATGCCTCCCAGACCAAGCTGGGCCCCGGGAATGCTGCCTCCCC
Nme1	NM_008704	ACAAAACAAAAAGGTGGGTCTGTTGACGCAGCCCTTCACTTCCAGGAACTTGGCAGGCAGGCTAAGACAAAAGGATCACAAGTTCAGT
Irf1	NM_008390	TGGCGCGGGCCCGAGGGGGTGGGGAGCACAGCTGCCTTGTACTTCCCCTTCGCCGCTTAGCTCTACAACAGCCTGATTTCCC
Tcam1	NM_029467	GCCCTTGGGGGAGGCGGCCTTTTCCCGGAGGAGCGGGAGCGGAAGCTGCACGCGGAAGCGCGGAGG
Ddx5	NM_007840	CAAAGCACGCTGGGAGCCGCTCTATGACCTAATCACCCCGCCCCCCTGGCTCGGAGGCCCTCAACGCC
Ccdc45	NM_177088	CAAAGCACGCTGGGAGCCGCTCTATGACCTAATCACCCCGCCCCCCTGGCTCGGAGGCCCTCAACGCC
Vdac1	NM_011694	GTGTATGACCGTGGGCCCGAGAGCGCTCTTGAATAAGAGTCCTCTTGCAGTTTGCAGCAAGACCGTTTCT
Asb16	NM_148953	GCGAATGGGGCGTAGTTTCCCAAAAGTCTCATCCCTTCAGTCTCCACTTCCAAGGTCAAA
Pnpt1	NM_027869	CAGAAAGCCTGCAAGGATTGCTTTCCCGGCAGTTTGCAGGCTCCACGGAAACGAAACTGCGTCCGACTCCGCCC
Gfpt2	NM_013529	TTGGGCCAGGTCTTTTCTCAGGAGATGAGGGGGCTGGAGAACAGAGAGGAGAGGAGGAGACAGCCGGGAA
Trim25	NM_009546	TCTTTGGTCATTTGAGCCTACACACAGTAGGCCTCTGGCTCCCCCACCCCCACCCTTAACCTTTGATCTGCACACATTCCTGCACTAAGCT
Socs3	NM_007707	CTGGCTCAGGTCTCTAATCCCTGAGATCAAAAGGTAGAGGCAGGAGGACCAGAAGTTCAAGGT
Xpo1	NM_001035226	GGCCCAGGTTCCAAACGCTCCGCGGCGCCATGGGCTGAAAACTCAACCGAGATGGAATCTCCCAGTCTGAACCGGT

Xpo1	NM_134014	GGCCCAGGTTCCAAACGCTCCGCGGCGCCATGGGCTGAAAACTCAACCGAGATGGAATCTCCCAGTCTGAACCGGT
Cyb561	NM_007805	CGGGTTCGGCGCCCGGGTTCCCGGTCTCTAGCTTCTCGCTCGCTACTCTCCACGCCCAAAC
Slc16a6	NM_134038	CGCCCGCGCCCCGGCCCCGCTTCTCTCTGCCTATCTCTTATCCTATACCGGCTGCAGCCGGTCTCCGCCG
Slc16a6	NM_001029842	CGCCCGCGCCCCGGCCCCGCTTCTCTCTGCCTATCTCTTATCCTATACCGGCTGCAGCCGGTCTCCGCCG
Rnf185	NM_145355	TGAACCTCCGACCCCTCCTACCGGGAACTTGGTCACCTGACGCGGAGCCGCCTCTAGTAGAACAACTTCCGGTTCCAGCCGGAAAAGGC
8430429K09Rik	NM_027820	TGAACCTCCGACCCCTCCTACCGGGAACTTGGTCACCTGACGCGGAGCCGCCTCTAGTAGAACAACTTCCGGTTCCAGCCGGAAAAGGC
Fignl1	NM_021891	GAGGTGTAGCCTCCGGGCCGCCACTCCAGAGCCTGCCCGCCCCGGCGCCCTCCGGCCTTAACCAGTTCAGCAGCAGCTATCAAATAGTGAGACTCGAATACAGGAAGG
2010316F05Rik	NM_026465	GCCCGCAGCTCCGAGCCTGCCATTTTCCCCTCTACGTGGGCAGGCTTACCGGAAGTGCCACGGCTTCGG
Scgb3a1	NM_054037	GGGAAATTGTGTTTTGTTTTTGCCATTTTTCATCATTGGTGATCAAATCCAGGGCCTTCCTTTTGTGAGACAAGTACTCCACTGGTGTGCTCTACGGTTCAGCCCAG
Scgb3a1	NM_170727	GGGAAATTGTGTTTTGTTTTTGCCATTTTTCATCATTGGTGATCAAATCCAGGGCCTTCCTTTTGTGAGACAAGTACTCCACTGGTGTGCTCTACGGTTCAGCCCAG
Wdr79	NM_144824	TCCAGGGATGCCTTCTTATGCAAATAGCCTCCCTGCTCTTGCAATCTCTTTGACTGGATTTAGTGAAG
Eif5a	NM_181582	CCACTGTGCTGCTTGCGGCGTCAAGAACGCATGCGTCTGAGCAGGCGCCACACCTCGGCTTTAACTGGAATTGAACAACTCACAAACACGTTTCTGAGAACCTTTCTA
Nr1d1	NM_145434	GGCCGCACGCGGCACTGGAGCAGGTACCATGTGATTCCAGGGAGCGCCTCGTGCCCCAGTGACACACTTTTCCAGCAGCCGGCACGTTGAGAT
Fasn	NM_007988	CGCGCCTCCCTGAGTTTCCGGGACCCTCTCCCTCCCTCCCTTTAAATTCCTCTTTTCAAAGGGTT
4930412M03Rik	NM_177098	ACCGGCAGCCAAGGCCCCGCCCCTGGTAGAGCCGGGCCCCTTTCCGGGATTGCAAAGCCG
Ndp52	NM_029755	CCCCACACCCTGCCCTGCCTGTAGACCCTGTCTCAAGGTCTGAATTCCGGGATCCAAGGGCTCAATTGCA
Tmem106a	NM_144830	GGCGTTGTCACCTGGTAAGGCGTCCCTGGGACCCCATCTCTTTACCCTTTTCAAAGCAAG
Rps27a	NM_001033865	TTAGAACTACTTGTCCCAGGATGCATTTCCACACTTCCCGGATACCTGATTACACTGTCTAAGCTGTGGAGTGAGGGTTAGGAGAGAGTCAGGTGAG

Rps27a	NM_024277	TTAGAACTACTTGTCCCAGGATGCATTTCCACACTTCCCGGATACCTGATTACACTGTCTAAGCTGTGGAGTGAGGGTTAGGAGAGAGTCAGGTGAG
Alkbh5	NM_172943	GGCAGTCCCGGGACGTGACTTGTGGAACGTCCGCTTCGGGAAGCGATGGCGGCGGGAATGGGGTGTGGGTGCCC
Rpain	NM_027186	CAGAATCCTTTGCGCGCGGCTAAGGGGCGGTGATTTGGGCGCTGTTTCCCGCTAAGGGAGGAGATGGCAGAGTCCTCGGGGTCTCCGCACCGCTTGTTGTAC
Nup88	NM_172394	CAGAATCCTTTGCGCGCGGCTAAGGGGCGGTGATTTGGGCGCTGTTTCCCGCTAAGGGAGGAGATGGCAGAGTCCTCGGGGTCTCCGCACCGCTTGTTGTAC
Flot2	NM_001040403	CCCTCTTTTCCGGGTGAGGCAGACCCGTTAATTCCGAGCAGGCTAGGGCTTGCCAGGAATTACTGCCATCACCCGCCCTGCAAACGCGGGTGC
Flot2	NM_008028	CCCTCTTTTCCGGGTGAGGCAGACCCGTTAATTCCGAGCAGGCTAGGGCTTGCCAGGAATTACTGCCATCACCCGCCCTGCAAACGCGGGTGC
Cdc42ep4	NM_020006	GAAAGTTCCCTAACTACTTAAAGGAAGTGGGGGTGGGGTGGTGTAGGCCTCAGCCTCCTTTTTCCCCAGAGTTGCCTCACGGTCCCTCAGCT
D230014K01Rik	NM_172573	ctcctttattttacaaattaaggtgggaagcaggtttactagaaatcacccgagtgctgactcactccttgttggcag
Fos	NM_010234	CCCTGCGCTGCACCCTCAGAGTTGGCTGCAGCCGGCGAGCTGTTCCCGTCAATCCCTCCCTCCTTTACACAGGAT
Mycn	NM_008709	TACATACACAGCAGGGGCTGTATGGTAAGTGTTCCTGGATGCCGCTGGAGGTAGGCTCCATTG
Odc1	NM_013614	GGAACCGATCGCGGCTGGTTTGAGCTGGTGCGTCTCCATGACGACGTGCTCGGCGTATAAGTAGCGGCGCGTCG
Sntg2	NM_172951	AACCCCGCCCATCAGCTCTGCCCTTCCACCTCCTGTCAGTGAGGGGTGAACTGGTTTGTG
Arf6	NM_007481	CCAACTCGAGTACAAAAAGTGCGGGCTACTTTGGCGGATTCTATGGAACACTGGCCTCCCA
4930534B04Rik	NM_181815	TGAACTAGCCGCCCAGGCACCGCTAGAGCACAAGACGCGCCGCCGCCGCCTGGCCCTCTGGGAGCTGTAGTCCATCCCACACTCC
Smoc1	NM_022316	GGAATTCCCATGGCCCGAGCTCCCGCATCCAACCTGCTGTCGCCGCGGCCACGCCGAGCGCAGCAGGCGCCACGCGCAGAGCACACGC
Adck1	NM_028105	GGTGGCGAAAGCACTGTTTCCTGGAATTTGGGTTCCGGGCTGCGCGGCGCAGCTTCCCTACCCTCTGGTGAGTAGCACCCGCGCACAGAGTCCTGGCCAAT
Ankmy2	NM_178910	TGGGTGGCCAGGAAAGGCAGAGAATTCCAGGAAGAGAAAAAAAGAGGAACAAAGGGTGGAAA
Ankmy2	NM_146033	TGGGTGGCCAGGAAAGGCAGAGAATTCCAGGAAGAGAAAAAAAGAGGAACAAAGGGTGGAAA
Twistnb	NM_172253	TTGTGGACTGCAGATGAGTAGCCTGGTGAAGGTCAGTTCCCAGAGTCCTGCCAGTTGTTTCCGGGAGAATGATCTGTCCTCCGGAGAGCACTGGGTGTGAGCTGTGC

1200003C05Rik	NM_024205	GAAGCAGGTTTACAGGAACTCATCTGAGTGCTGACTCATTCCTCGTTCGCAGTCCCTCACCGGAGAACAGAATTG
Ckb	NM_021273	AGAGCCACAGAGCCGCCGACCTTCCTCAAGGTGCCTGCGGGCATCTCCTGGGTGTTCTTGGTGCAACACCAGAGG
Brf1	NM_028193	TGTGCGGCCAAGGCCCGGCCCGTGGAGCCTGCACTGATTGGCACAATAGGCTTTGGGAGCGTCCTGGGCTGGATGTAGTGGGAGTAACTTGGGGAGTCAGCAAGCCCTAGAGGGCAGGATCAAGGACTGCCGGCG
Nup153	NM_175749	GGAGCCTCTGGGAAATGTAGTTTTTCTGGCCAGAACGCGGATTCTCGGAAAGGCAGGCTA
Map3k1	NM_011945	TCTCCCCACCCCCAACAGATGCTCCCAGCTGCACGTCCCTCTTCCTGGCAGTCAGGTGACA
Tmed9	NM_026211	GGCCAAGCAGCCCCTTTTATAGAGCCAGGACTACCTGACTGTTGCCAGGTAACTGTGGGGCG
Il6st	NM_010560	GCTCAGCCTCCGGAATCCCGGACGCCGGGAGCCGCGTTACGGGAATCGCAGAGGCCTGCAGTCCCGCCCCTTC
Hist1h4a	NM_178192	ACATCACAAACCCCGCCCCTCAGCCAAGACCCGAAAGCGCGCCGGCGGGAAAGCGACATCACTGATCCCTCCTCT
Hist1h1a	NM_030609	ACATCACAAACCCCGCCCCTCAGCCAAGACCCGAAAGCGCGCCGGCGGGAAAGCGACATCACTGATCCCTCCTCT
Cart	NM_013732	TTGAAATCGGGTGCCGGGAAGAGGGAGGGGGAGAAGAAGGACGGGGGTGTGGAGGAGAGCCCGGG
Hist1h2bb	NM_175664	CCCTCTTCTGAGTTTCTCATTTCCTCCTGGGTCCTGGTGAAATGAACTCTAGTTTCTGGAAATACCTCACTGA
Ippk	NM_199056	CCGCGTTTCGGAAGTGAGTCACTCTGCCAGCACATAATATGGCTTCCACTCCACCTACCACCCTGGACGTCGAGGGTAAGGTGGGCGGG
Hist1h4k	NM_178211	CCTGCAGGGAAGAGGCGGGAAGTTGCGCCCGCAGCTGTGGGGGAGGGGAAGACTTACCAA
Hist1h2bn	NM_178201	CCTGCAGGGAAGAGGCGGGAAGTTGCGCCCGCAGCTGTGGGGGAGGGGAAGACTTACCAA
Peci	NM_011868	GGAGGCTTAGGCCCAGCAGAAACTGCAGGGCAAGACCGGGAAGGGGCGGAGCCAGAGGTGCGCTC
Arsk	NM_029847	GGTGTCTGCTCCCCGTCCTTTGGGTACTTACGAAGGAGTCACTGGCGACCAGCACCACGTTGGGCGCCTGGTTC
Eef1e1	NM_025380	GGTGTGTCGCCAGAATGAGCAGGGTCCTATTCCGTGTTCCCTCCGCCAGGCGGCTTCCAGGAATCTGTACCGCTCGCCC
Zfp459	NM_177811	AGGAATCTTCAGCATCACAGGACTCCAGTCCAACTTTCGGGAAGATTGACGAGTGTTGACCAAAAGCCGGGTGGGATTTGCTTGTGACGTCGGAGTCACGTGGGTAC
Atg10	NM_025770	GTTGTGTTGGCTGCAAATCTGAAAAGCCTGCCAGTCACTTAACTTCCTTTGTTTCAAGGTCACG
Elovl7	NM_029001	GGGAACCGGCCCCCTACTGCACCCTGGGTTGCTCGGGGCCAGGCTCTACCCGCGGCGAGGGCGGCAGCGGGAGAGGCTGGCATGACACCCCACCCCTCGGCGT

		CA
Arl15	NM_172595	CCCCAGTACTGCACAGTTTGCCTTCTTTAAGGTGTCTGCCCTTCTAATCCGCAGGTCCAGGGCGTTTCAAGGCCACAGGAAGGCGCTCGGGGCAACTGC
Isgf3g	NM_008394	TCCCTCTGGTGGTAACCGCTTGCCCTGCAACTCAGACCACGTGGTTTCTAGGAAATGCACCTCCCCGGA
Zfp219	NM_027248	CTCTAGACATTGCTTTCCAGGAAAAGGTCAGTTTGCCTGCGGGGGGGTGGGGGTGGGGGGGGATATTTTGCAATACT
Spry2	NM_011897	GGGAGGGAAAGGGGAGCGGGAAGTGAGGTGGGAGGGCTATTGGTTTATTCTTTGTCTACTG
Gzmc	NM_010371	GTCCTGCCTTCCCCACTTTTCCCTACTGCCTGCTACAGTATGTGGAAGACCAACTGTGTGCTACA
Sncg	NM_011430	GCCTCCCCACAACCCCCTTCTGTGTCTCCAGGGATTCGGCCTCTGCACATTTCCAGGAGTGGGAGGAGGGCCTGAC
D14Ertd436e	NM_172599	GTTTTCCGGGGTCATTCTGGGAAGGGAGTGTTCCTCACAACCTTACAACCTTCTAGCAGAAGGTCCCCAGCGTGCTACTCTAGCAAGGACTTTCAGCGGTCATCTTTTGTTCTCTAAGGTCACACATTCCCACAGGT
E430028B21Rik	NM_178668	GTGACTGGGCGGTGCCTCCGGGAAACACTAGGCTTTCTGTCATTTCCAGTTGCTCCGGTTATGGCTGTGTGT
Ednrb	NM_007904	GAGCACCCTGCACATGGATTGACGTTGCTCTGCCATATGTGGATGAGATGTGGTGAGCTGCCTGAGATCATGCCTTGACTTGCCCTCAGTGATGAAAGTCAAATCACCCTTTCCTTCCCGAG
Slc15a1	NM_053079	CACCCTTTAAGGGTTGATGAGTCTTCCACATTCGCTTTGTTTATTCAATCACCTGCCCTTAGGAACTCCCAGCCACCCTG
Tep1	NM_009351	GACTGGTTGGAAGCAGAGAACTGAAAGAAAACCAACACCCTAGTGAGGCCAAGGGGTGAGGCTG
Pnma2	NM_175498	TCCCTCCCTGCCCACGCCCCCCGGCGCCGCCACGCCACCTCCGAGCAAAGTTGGATCTGAGCGGGCGGTCGCTGCGGCAGAGGATGCCAGTTCCCGGCAACGCGGGGCGGGGCGGAGTGGGGCGGGGCAGGAGGAACGCAG
Dcp1a	NM_133761	CAGCGGATGAGATTAGCTGAAGTACCACGCTCGGCAAGGCTGGGCCGGTAGGCGGAAGTGGAGGGCTGA
C130032J12Rik	NM_178684	GAGCGGGCGACCCTCCCCCACATCCGCCTGCGTGACCGGCTGGGGGCTGGTTCGCTCCGGTTGATCCCGGATTCCCTTTGTTCCCTT
C1qtnf9	NM_183175	CCACTGAGGGTGAGCTCCTGCCCTTCAGAACAGAACAGTATCCTTATGCTCTTGAAACCGCTGCACGTTTGCCTGACCGTTAAGACAC
Clybl	NM_029556	AGGCGGGGCGAGGGCGGGGCGTAGGCGGGCCAGTCGGGAAGATGGCGTTGTGCGTGCTGCGGAACACGG
Vps28	NM_025842	GGTGCTCGCTTTTTCCGCCTGCGCCTGCCGGGAAACCCGATCGGCAGCTCGGCACTCATCC

Naprt1	NM_172607	TCCACCCCCTACGGCACTGGTCCAGAGAACCAACTCACACGAAAGGAGGGCCTTTCCCGGCAG
Pabpc1	NM_008774	GGAGAGGTGGCGGCGGCTGCCGCTGCTGCGGGCGTGGGGGTTGGGCCCGAGGCGGGGCGGGGCTTC
Oplah	NM_153122	CTTGCTTGTGTCCCGCTGCGCTTCCCGAAGGCCCTGCCCCCACCTCGGGGTGGGGCCTGGAGAA
Mtmr12	NM_172958	ACTAGGAGATGCCCCCACCCACCCTGTTAATCCTTCCTGGAAATGCTCTTGTAGAACTGCCCATA
Sh3bp1	NM_009164	GTCCTGCCTCAGCCCCACCCCAGGGTTCCTGGAAAGGCCTTTTGAACTGTGGAAGTGGGGGTGGGCAAGG
Ptk9	NM_008971	TGTCGTCACAAGCCCCGCCCCTTAAGCCATTGGCCATGCCCTTTCCCGGCAATCACCCCC
Cbx5	NM_007626	GGGAAGTGGAGTTGGGAAAGGAGTAAAGACGGAGAAGGGGGAGGGGAGGGAGGGAGGACAGG
Amacr	NM_008537	CCAACTGATCCAATGCTAGGGTGGGCAGGAAGTGCGCAAGCGCGCAGCCTTCCCGGACGGGGC
AK162044	NM_177597	CAGGGATGCCTACCTCGCCCTCATCCTTACTCCCACGCGGGTCTCTGCTTGGCCCACCGCGC
Myc	NM_010849	AGGAAGCATCTTCCCAGAACCTGGAAACCCTGCAGCCCTGCCCCCATCCGACCTCCGCCCTCGTTGGCTTCGCAACGCTG
1700088E04Rik	NM_138581	AGAAACTCCAAGGAGCTAGAGTGTCAGCGTCCTCACTAATCGCTCCTTGTTACCATGGTAACTAGCGACACGCCTCCACGCACGCGCATTAGCGT
Polr2f	NM_027231	AGAAACTCCAAGGAGCTAGAGTGTCAGCGTCCTCACTAATCGCTCCTTGTTACCATGGTAACTAGCGACACGCCTCCACGCACGCGCATTAGCGT
Ropn1l	NM_145852	CATGGTGTCGGGCAGCGGCATCGTTCTGGGGAGACCGCGGCGGCCTGGGACGTTGTGCTGCGGGGAGGAGAGGCAGGGT
Myc	NM_010849	CCTCCCCCTTTCTGGGAAGTCCGGGTTTTCCCCAACCCCCCAATTCATGGCATATTCTCGCGTCTAGCGCCTTGATTTTCCCCACCCCA
Apobec3	NM_030255	GGGACAAAGAGGTGGGCAGGAGCCTTCTGGGCTTGATCGCCTAGAGCCCTCCCATTCCGGGAGCTG
Mettl7a	NM_027334	CCCGTGACCTGGATGACCCTGCACTGAGCTGCACTACAACACCTGAATTCCAGCGCTCCTACAGTCATGTGGGAAGCAAAGACAGAACTGCACGAAAGCCAGTAAGTCAGCTGGT
Cox6c	NM_053071	AAGACATCCTAGTTCGCCGCCCCCACGAGAAGCCGAGAAACCCGCAGTTGTCAAACCCCAGAATCTCCTCTCTCTCTCCACCATTCTCACCTCTACACCAACGTCCTTCCCGGTTCTCGGAGAAACGGAGA
Zfp406	NM_198644	CAGGCGCGCAGGGCGCTCCCCTCGCTTGCTCTCCACCGCCTCCCTTTTTTTTCTTTCCTGCGGCAGGATCAAGCCAGCTTCCAAACG
Jrk	NM_008415	TGCGGACCCCGTGCCGCCGCTACCGGCCGGAAACGCCAGCCACGCAGCTCTCCACCGGCCCGCTCTTCTCGGCCTTCCCCGACCCACTTCC
4933427E11Rik	NM_025756	TGCGGACCCCGTGCCGCCGCTACCGGCCGGAAACGCCAGCCACGCAGCTCTCCACCGGCCCGCTCTTCTCGGCCTTCCCCGACCCACTTCC

Aaas	NM_153416	CGGGTTTCGGGACGGACTTCCGGGACTTCCTGGCGCGCCCCCTTGCGTACGGAGCGGGCACGACGCTGACACGTCCGAGGACCGACCTGTGGCGTAAGGA
Chrd	NM_009893	CCCTTTCCCTGCTCTGTCCTGCTCCTCCCATTCTGGGAAGGCTCCACTCTTCTTGACAAAGGTCAGTGCCTGTA
Prodh	NM_011172	TGGGTTAGCCACGCCCTGGGGCCACGCCCCGATCACGCCCCATTCCCGGAAGCCCCACCT
Liph	NM_153404	GAACCTGCCCTGGAATGTGCCGCTCCCTGCTGGGTCAGTGTACCCACCTGATAAGTATTTGTTGA
Bcl6	NM_009744	GAACCCCAGTTCTAAGAATCAACAGAGCTCAATTCTCGGAATTTGAGCTGCGGGCTTTACCATTGC
5730409G15Rik	NM_027446	AGGCGGACCGGGCCGGGTTGGGCCTGACTGGGGAGCGTTTTAAACAGTTCCTGGAGCTGGAGCTGGCAACTTGGAGGCGAAGCCT
Lpp	NM_178665	TGCCTAGCTCTAACTTGGGTCTAAGCTCACAGTTAGAGGCCGGGTCGTGCCTGGAGGCGGAAA
Coro7	NM_030205	AAGATGTAATTTTCAGGGTCAAGGGAGGGCATCCACACGGGGTATACCGGAATCTGATACTG
Dnaja3	NM_023646	AAGATGTAATTTTCAGGGTCAAGGGAGGGCATCCACACGGGGTATACCGGAATCTGATACTG
Fyttd1	NM_027226	CAGGGCCAGGCTAGTCGTTCAGACTCGGTTTCGGAGGCGCTGCCAATGGTGTGGACCGTCGA
Rrn3	NM_001039521	TGGTGTAAGACTGTGGGCCCCAGAGTGCTCTTGGAATAAAAGTTCTCTTGCGGTTTGCATCAAGACCATTTCTTATGAGTGATTTGGGGTGTTGCCTCTCCTGAGTCAGAACGT
Pros1	NM_011173	CCCTCCCCACCCCACCCCCGCCCCCCAGCTGCGAAGAGCTTCCAGGAAATGTCCCAGTCACCGCTTCCCCTCCCGGGCTGGGGGCTGGGAG
Ube2l3	NM_009456	GGTAGGCCAGGCGGCTAGAACCCCCTCACTTCCTGGAGCGGGGGAGGGGCTAACCGGGAA
Eif2b5	NM_172265	ACCTCCCAGTAGCACCTACTGCGGTCAGCCACGCCCTGGTCTTGCACGGGGTGGGTGGGGT
Trap1	NM_026508	TGCCTGTGCGAGAACGGGAACGCAGCAAACCGCAGCGCGGGGGCCCTGAAGACTGTACTTTTTGA
Dnajb11	NM_026400	CACGTACTTTGACACCTCCTGGGGTTGCACTTCGGTGAGCGCTCGCAAGTCACGTGTGCACA
Ifitm7	NM_028968	CCCCACATACAGAAATGGGGGAGTGTCTGTGTGCTCTTTCAGCCTTGAGGTTCAGAGCATAGCTGA
Morc1	NM_010816	ATCTCCATGAGAAGAGCCACATAGCAGGCTGAGCTTCAGCGCTGAGAACACCAGGGGGCGAAGGCGTCTGTTGAGCTCCCACTCTGCAAGTGAGCCAGGCCGTACGCGTGGACGTAGGCGTGGGCGT
Tfg	NM_019678	GCCCGGCTTCCTCACTGGATGACCGAGTGTAGGAAGTGCGAGCCGAGGCGGACACGCATG
Pou5f1	NM_013633	CCTCCCCCCAGGGAGGTTGAGAGTTCTGGGCAGACGGCAGATGCATAACAAAGGTGCATG
E130307M08Rik	NM_026530	CCCAGGGCCTTGGGCGCCTAGTAACACCGCCCCTTCCCGCTCGCTGATTACACGTGAACGC
AW049765	NM_145934	CCCAGGGCCTTGGGCGCCTAGTAACACCGCCCCTTCCCGCTCGCTGATTACACGTGAACGC

Zfp13	NM_011747	GGAAGCCCCTTTATCCCCTTACCTGAAAGGGATGGGTCAGGCAGGGAACTTCCTGTTCCATTTCCCGG
Zfp206	NM_001033425	GGAAGCCCCTTTATCCCCTTACCTGAAAGGGATGGGTCAGGCAGGGAACTTCCTGTTCCATTTCCCGG
Ly6g6d	NM_033478	CCTCTAGGGCAGGGGAGGGTTCAGAGTGTGACCTTGAGAGGCTCTGACGGGAAACAGACAAAACAAAA
Ly6g6e	NM_027366	CCTCTAGGGCAGGGGAGGGTTCAGAGTGTGACCTTGAGAGGCTCTGACGGGAAACAGACAAAACAAAA
Stk38	NM_134115	TTTTTCTTTTGAAATAATTATAGACTCGCCAGAAGTTACAAAACGAAAACCTGGAAGTTCCGTAAAAGCCAACACCCACCCA
Lama1	NM_008480	GACAATAGAGACACTCTGATATATCTGGGAAAGCATTCTCTAAGAGTTACTGTCAAAGACAAGGTCTAAATG
Tmem8	NM_021793	ACTGTGTGCTGACTACTAGGCCAACACAATACAGTACGTTTTTGCATTTGCTGTTCCCTAATTTCCTGGAAGGGTTC
LOC547127	NM_001045538	TCTTGGTGTCTTGCGCACAGGCGTGCTCACACAGACACTGTCTGACCCCATCCCCACCCC
Pde9a	NM_008804	GAATGCACAGGCTGCTTGGGGAAGGAACTTTCCCCACTTCCGATTCAAATTAAGTGAGGGTGGCCTTT
Pim1	NM_008842	CCCGCCACACCAACGCCCTTCCATTTCTCACAACTTGCTACGCTCCAGCTCCAATCCTCGACCCCCCTCCACAACCCAAATCTCCGGGAAACACAGAGCCGGCAGAG
Stk19	NM_019442	GCCAGGAGCCGTCTCTTGCGATTCATAACCCGGATTTCAGGATTCCGGGAAAGGAGTCCCGAAGACCG
Dom3z	NM_033613	GCCAGGAGCCGTCTCTTGCGATTCATAACCCGGATTTCAGGATTCCGGGAAAGGAGTCCCGAAGACCG
Flot1	NM_008027	GGCATCCCCCTGGGCTGCCGAGAACTGTAGTGCTGCGGACCCGAGCGGAGCCTGCCGGGAAAGGGGCGGACCGAGGG
Nrtn	NM_008738	GCCCCTGCCACACCTGGTTGCCGAGAAACCAGGGTTGAGGCTCCTCCCTCTTTGACATCCTTTGCCAAATCTTCAGCTCC
6330416L07Rik	NM_176962	TGGAGCTCCGGGCGACACTATCTCCCTCAGGAGACAGAGGTGTCAACCATGAGGCTCAGAAG
Pknox1	NM_016670	CATCCTGGGAACCCCTCCATACCTTCCCTTTCTCCTCATGTTCCTATCCTGTGCTGCCTCTGGTGTCTCTCCTACT
Pou5f1	NM_013633	ACACCGGAGTCCCTGGAGGAAGGGAAGCAGGGTATCTCCATCTGAGGCTCTGTCTTTGAG
Riok2	NM_025934	TCCTCCTAACCCGTCCTGGGATCAGCGTCCCAGGCCAGCGGGGCAGCTCCTAACCCGGCCCTCCTCCGCCGGACAGGGGTGG
BC049807	NM_001002008	AGAACCGGAGCCAGGCGGCCCTGGAACCGCCCAGGTCAGAGGAGCTGTGGGGTTGGAAAAGGGCGGGAAGGGAACAGGGTGTGATCGGTTTG
Hcfc1r1	NM_181821	GTGGTAGGAATCAGGGTTGAGGGTACCTGAAGATGGCAATCTGCCCGTAATTGTTGCCAGCTGCCAGAAACTTCCCGCAGGGGGAGACACT
Rps10	NM_025963	TCTGCTCTCCTTTGTGACCTTTGCCGGCTCCATCTGAATCTTTCCCGACAACTGTGCTCCCCAACCCCCACGCTTGGCTTCATCTCAGT

Cdkn1a	NM_007669	TCAGTGCAGGGTGGTGGAGACCTGATGATACCCAACTACCAGCTGTGGGGTGAGGAGGAGC
Rab5a	NM_025887	CTGAAGTGGTGTGAGAGGCCTGTGAGTGAACCATCAGACCGAAAATCGCCGCAATGGGAAG
Zfp13	NM_011747	CAGTGCAGCAGCGCTCCTTGTGTGGTGCTGCTCTGGGCTGCAGTTACTGGAATGGAAAGTTCTGCCTAAGGCTCTGGTCCCATCCCCCTATCGGAACTCCCACTGTTTGGGGGGTTGG
Pnpla1	NM_001034885	GGCAAGTCTATAGGGTATTTTCTTGATTAATGATTGATGGAAGAAGGCTCAGCCCACTGTGGGCGGTGCCATTCCT
Rps28	NM_016844	TGAATGGCATGGACCCCAAGTTGGCTTGAAGGCTGTAAGGGAAAGGAGTTGCACGGATTTACT
H2-T24	NM_008207	GGTGGGGAAGTGATGAAGCTGGGAAGTCGAAACCGAAACTGTAGCACTTTTCTACTGCTG
Calm2	NM_007589	CTTTCCCCGACCCGCGGGGCGCCGGCCGCTCAGCTACGCACTCACCATGCTGCAAGGGCTACGGGTTTCCGAGACGCGACCAGACAACCGCTCGAC
1600002H07Rik	NM_028056	CATTTTTGCCGCCGCCAAGGAGTCCCGCGCCTTCCGGGCAGAAGGCCGCCCACTTCCGGGTAGGCTACCCAATCTTGAGCACAGCTTGC
U2af1	NM_024187	CTTAGGCTGTGGACAGCCGCTCCGCGCGTGCTCAGCACCGCTGTTTCCCGCTCCCGCCGCTGGGACCGCGCCCTCTCCCCTTGCTG
Pou5f1	NM_013633	GGGCAGGCATTATAGGTGTGGCATTCCGCATCTGGCTTCCCAGGATACCTTTTCATGCTGGTGGACCATCTCTGGCTGGGGACGTG
Tubb5	NM_011655	CTTGGAATGACTTCTATGATAGAGCCCTTCTAGCCGCCGCCGGTAACTGGCGCCAGACTCTCTGGTAGGCGTTTGGAAATCTGCGCGGGAAGTAGTCCGTGGATGACGTAGCGACGGAGG
Gna-rs1	NM_008136	TTAGGGGTCCATCCCTTCTCCAGGGCTTAAAACATGAATCAGGGCCCAATTTCTCCTCACCTGACTTGGGATCACCAGGCTTCCCGTTAGCCATGGGGGGAGGGCCCAGAAGGCTGGGTGGTCCTAAGAGCAGACGTGAGAAAACAGCCATCAGA
2410137M14Rik	NM_029747	GAGGTGCCTGTTTAACATACCAAAGTGGAGTGGCCTCCAGATTCTTCTGTCCTTGAGTACCTACCCTCAACAGGGTATGGCTGAAGTA
Spats1	NM_027649	GGGTTTGAATGTCCTGCCCACTCCTCCTCCTCCTGACTCAGGGCTCCCGAAAGTACTCGCCCCGCCCCGTCCTTGGGTCTCCTTTCCACCTCTGAGTCCCACCCTAC
Spats1	NM_027649	CTTCCAGCCGCTTGCATGGCACTCATTGTCTTCAAAAGCTCTAGGGAACTCTAAATGATCTTGCCCCTGATCGGAAGAGGAACACTTTCCTGGCA
E130307M08Rik	NM_026530	TGAGGTTCTGCCCTGACCACGCCCCCAGGCCCCCCACTAAGAACGGTCTTGAGAGGGCCTGGGCGCCTGGCTTGTGGTGGTAG
AW049765	NM_145934	TGAGGTTCTGCCCTGACCACGCCCCCAGGCCCCCCACTAAGAACGGTCTTGAGAGGGCCTGGGCGCCTGGCTTGTGGTGGTAG
Fbxo15	NM_015798	GCTAAAATGGCACGCAGCCACCGCCCTTAGTTCCCAGATGTGCTTTATCATAACAATGGAATTCC

Eif1a	NM_010120	GGGCCAGTGCCGGGAAGTCGACGGAAAGGGGCGTGGCCGGCCGTTGCCTAGGAAGGGCGCGT
Osbpl1a	NM_207530	CTGTCCGCCTCCGCCGTGGGGCGGAGCCTCTCCCTCCTTTCTCGGAAAGCAGCAGCGGACTAG
Wdr55	NM_026464	GTCTTAGAGGAAGCTGCACGCTGCGCTCGCTTAATTCGCATCAGCTGCGGCAGGCCCGCCTCTTCTGAAATCCTCCCAGTGCACTTCCG
Tcf4	NM_013685	GGAACGGGGCGCCAAGCGCGCTCCGAGAGCCACGACCTGAGTGAGTCCCACCCGCCGGCGGGACCGCCCTGG
Ccdc68	NM_201362	GAGGCTAAAACTTCCAGGCAGTGGAGAGCCAGAGGCTCCTCCCCGAGGTCGGGGACACTGGACTCTGGCCTGGGCG
Slc6a7	NM_201353	CTGCCGTGAGGCCGCTGCGGGCGTGGGGTGCTACGAACGCCCTGCCTCTCCCTGCGCAGCGCCCTAGG
Lman1	NM_027400	GGGGCGTGGACGGGGTCAAGGACGGATACTCGGTATAGTAGAGGTGCGGTGTGTCCAGCTCTGTAGTGCCTTTGGGGGAAGGTGATTAC
5133400G04Rik	NM_029485	CATCACTGTGGACAGCTCCCACAGCTCCTGTGATAGCTGTAGGCTGAGGAGATACCATAGTGCCAC
5133400G04Rik	NM_027733	CATCACTGTGGACAGCTCCCACAGCTCCTGTGATAGCTGTAGGCTGAGGAGATACCATAGTGCCAC
Cxxc1	NM_028868	CTGCGTCGCAACGTCGAAGCAAATGCGGCCATATTGCCCTCTGGCGGCCACCGTACGGAC
Pura	NM_008989	CACTTCCTGTCAATGGTTCCTGGAGCAAAAGCCTGCTCATCTAGCCTCTCTGCTTTATGCTAATTTCTCCCCTCAATCCCCTCTCGGCGGGCGTCTCAAGGCCAAGGTGAGACCCTCCCCGGAGATGAAAGGCTCGCTGC
Napg	NM_028017	AGCCCCGCCCTCTCCGCGCATTCATTCCACCCATTTCCGGGACAGCTTTGCCACAGGAAGTTTGAGTCCTTCGCTTCCCGTAGTCCCCTT
Smad7	NM_001042660	CGGGCGAGCTCTGCTGGTCTAAATCGGGCCACTAACCGGCTCATTCCGCTCCAAACTCGCCCGC
Ier3ip1	NM_025409	CCTAGCTGAGCGTCCGGTGCGTGAGAGACTGTGTCAGGGGAATGAGGCAGAGAAGGATAGAAGACACCG
Ccdc5	NM_146089	AGGTAGGCAGGAGGAGACTCTGATTCCACACTGGATTGGAGTGTAGGCACAGGAGACATCA
Atp5a1	NM_007505	AGGTAGGCAGGAGGAGACTCTGATTCCACACTGGATTGGAGTGTAGGCACAGGAGACATCA
Tut1	NM_197993	GAGCTGGAACTCTCAATCCTACGAACGAGGTTTCTGGAGGAATATGGCAGCAAAGGACACGA
Dak	NM_145496	CTGCCTGCGTACCGGTACTCTCGCTCTCATCCGGGTACTGCGACCTCTGGCGGTTAGGAG
Ddb1	NM_015735	CTGCCTGCGTACCGGTACTCTCGCTCTCATCCGGGTACTGCGACCTCTGGCGGTTAGGAG
Rab3il1	NM_144538	CTTTGCTCACATTGTCTGGGGCCTGCTTGCTCAAGGTCATCCTGTGGAGCGCCTGCAAAAG
Hells	NM_008234	CTCCCCCAGCTACTGCTGGCCTCCTCTTCCAGTAGAGATTTAAATAATAATGAAAGACTTC

Lgals12	NM_019516	GATCTGGGTCCCCAAGGCTAGTGGTGCCCTTCCCCCACCCCACATCAGCCCTGCTGGGAAATGAGGGAGGAGGGTGCACT
Hrasls5	NM_025731	GATCTGGGTCCCCAAGGCTAGTGGTGCCCTTCCCCCACCCCACATCAGCCCTGCTGGGAAATGAGGGAGGAGGGTGCACT
Klf9	NM_010638	CGGGAAAGGGCGAGGTGAGGATCTATCCCAATGTGAGGTCTGACACGTGATCCTCTACCCCCAGCGGGCCATCTGTTCTTTTTCCT
Gldc	NM_138595	TGAGCCAAAGAAACCCTTCCTCCCTTAAGTCGCTTCTATCAGAGCTTCATCACAGCAAGGAGAAAAGAGACAGAGGCAGTGCATAACCTCGACCAGGAGTGGCTCT
1810055G02Rik	NM_028077	CCTCTTCTCCCCGGCTTCTGGGAAAAGCCCTAGACACAGACATAGCCTACAAGTCCCTGG
Efemp2	NM_021474	AGATGGAAAGAGGTTGGGTAAGGGAAAGTTAAGGAAGACCTGGTTATTGCCGCTAGCGGTCTGGGCCAGGCACG
Ppp2r5b	NM_198168	GATTAACAATTTGCATTTGGCTTAGGACCCCAGGAAAGCAGACCTGGCCTCTAGGTTCTCCCAGCATCCCTCAGTTCCTTCCTGGCATACCC
1810013C15Rik	NM_194348	GATTAACAATTTGCATTTGGCTTAGGACCCCAGGAAAGCAGACCTGGCCTCTAGGTTCTCCCAGCATCCCTCAGTTCCTTCCTGGCATACCC
Ubtd1	NM_145500	AGCGCACGCTACTTCCAGGAAGGCAAGAGGCCGGAGCGTAACCCTTGGAACCCAGACCTTCTCACCTAACACTCCGCAAACAACGCGGTCCTGCGGTGCAAGCACCAGGTTTGGACCAGAACACCCGA
Mms19l	NM_028152	ACGGCCCCTCCCCAGAGGGCGGGGCCTGGGCCGGGGCGCGGCTCCGGGAGGGGAAGTGACTGCC
Ubtd1	NM_145500	ACGGCCCCTCCCCAGAGGGCGGGGCCTGGGCCGGGGCGCGGCTCCGGGAGGGGAAGTGACTGCC
Gm962	NM_001033448	CCCCTCAACTGTAACAGGGTTTAATAATCCTTTCTGGCTACCGAGAGCTGGGACACCAGACC
Nolc1	NM_001039351	TTGGAAATCTACAGTAGGAAGAAGCCCATTCAGCAAAGGTAATGCGCGGGAATTTGCAAGTTTTCCCGCCTCGGACAGGAGCGTGGC
Nolc1	NM_001039352	TTGGAAATCTACAGTAGGAAGAAGCCCATTCAGCAAAGGTAATGCGCGGGAATTTGCAAGTTTTCCCGCCTCGGACAGGAGCGTGGC
Nolc1	NM_001039353	TTGGAAATCTACAGTAGGAAGAAGCCCATTCAGCAAAGGTAATGCGCGGGAATTTGCAAGTTTTCCCGCCTCGGACAGGAGCGTGGC
Nolc1	NM_053086	TTGGAAATCTACAGTAGGAAGAAGCCCATTCAGCAAAGGTAATGCGCGGGAATTTGCAAGTTTTCCCGCCTCGGACAGGAGCGTGGC
Zdhhc6	NM_001033573	GCCGGGGGCCGCGGAACGCCGCCTGGGCACGCGGGGCTCGCTGGCGCGAGGCTGCTGTGGGTGGTGCTG
Zdhhc6	NM_025883	GCCGGGGGCCGCGGAACGCCGCCTGGGCACGCGGGGCTCGCTGGCGCGAGGCTGCTGTGGGTGGTGCTG
Vti1a	NM_016862	GCCGGGGGCCGCGGAACGCCGCCTGGGCACGCGGGGCTCGCTGGCGCGAGGCTGCTGTGGGTGGTGCTG

Ddx3x	NM_010028	CCTTCCCCCTTTCTCCTCCCCGCCCTCCCGCAGTTTTCCCGTCCCTCCCTCCCATTCCCAGCACTAGTCAAGCGAGTTTC
G530011O06Rik	NM_001039559	GGTGTTATTTTGTTCGACTCGGGTACACACTTCTCCTGATAGGGACAAGACCTACCTTTAGAATG
G530011O06Rik	NM_001039559	GAATCTCCGAGGCAACTGTCAACTGACCTGTAATGAAAAGTACGCTCTACATGGAAGTCCACTCGAG

Appendix2

The sequence from chip-clone results

1、

GGTGGGGGGGAGTAGCTGCTGCCAGGTACGTCTCCCTCCAGAAACGACTCTGAGACCAGACAAAATTCGTGCGCTGCTCTCTTCAGGCAGTGGGGTGAGGACAGCACAAGACTGAGAGGGTGCTTGGAGGCGCCCACACTCCCGGCTCTCCTTGGCCATAACCCCACAAGCAGGGCTCCAGGCAGAGCACGGCAGTCCCCCTGGGATGAGAGGCAGAGACTGGAGTGAGGGGCTTAGGTGTGCATGTTGCTGGTGGGGAGTGCTTGGGACCTCTGCAAGCCTGTGGCTGAGGGTGAGGAGGTGCCGGAGGCTCACCAGAGAGCAGTGACTATAGGCCCTGTGCTGTTATCCGTCACTGCATAACCAATCAACACCGATTTAGTAGCTTTAAAAAACATGCATTTATTCTCAGTTTTGGGGGGTCAGGAGCCCACACACAATTCCGCTGGGTGGCTCGGGGTTTCAAGAGTGCCACCAAGGTGTTGGTATTTCTTTCTGAAGCTTGAGGTCCTCTTTGAAGGGCACGTGGTTGTTGGCAGAATTCAGTTCCTTGTGGCTGTAGGACTGAGGTCCCTGCTTTCTTGTTGGCTGGCAGCCTGGGGCCACTCACTGGTTCCCTGATACGAGGCCCCTCCCATGCCCCCCAACACCAAACACACCCAACAC

2、

TTGGTGGTGTCCTAAGATTTGGGATTTACCAAGTACTGAGAATAGGACCTTCAAAAAATATGAAATGCCAAGAGGATCTGTTTTAAAGCAATGGAATTATTTGAGAATTTTGAAAAATACAGATTCTCAGGACCCAGTCTGAATGAGAATCTCTGGGGAAGAGGCCAAGGAAACAGAATTCAGGTAAGCACCTTGGCTGCTTCCAGTGGTTGGCCAATTTGGATATCCCTGTTGTGTCCTAAATTATACCTAATTTGATTAAAGTTTTGGTGGCTGGGAGGTTTGCTAGTTGAAAAACACATACAGGAAAAAAAAAAATGTACAGGGGAGTGTATTGCTTTGGTGTAGTCGTTTAAGAGTTGACAAAAACCCAAACACACCCAACACAAA

3、

CGTTTTTGGGTATTAGGGTTTAGCACAAAGATTATAAAACTATAAACACAGCCTAAAATAAAATGATTTTTTGTACAACTCTTTGATAAGTAAGACTAATTTAATATTGTTGGTTTAATAAAAATAGCTGTATCTTCTGAGTTATTGACAAAATAACCATATATTTAAGGTTCTTAGGTGAACACCTGATATGCACAGGCTATAAAAATGGTTAACAGAGAAATAACTGATGACTAGCTTTGTCTAATATCTCAGTTTTAATAAGTAATCTAGGTATAATTATTAAAAATAAATTTTGTAAATGTAAATGGTATATGTGTTTATAAATAAGCTTTTTATGTAATTTAAAATATTAAAGTTTTATGGTATGTTAAATTAAACAACAGATATTCATTAAATGTCTGGTTCATTTCCCAATTTTTCTTTTTTTTTCGGAGACAGGGACCCCTCTCTGTCGCCCAGGCTGGAGTGCAATGGCACAATCACACTCATAGCAGCTTCGACCTCTCAGGCTCAAACAATCCTCCTGCCTCAGCCACCCATGTAACTGGAACCAAAAACACACACCAAACACACCCAACACAA

4、

GTGTTGTTTAAATCATATTCATCAGACATTAAATGAAAAACACAGCATGTTCCTACTTAAAACCCATTATATATTGTATAGTTTATTTATATATTAAAAAAGGGACTTTACATTTATATATCAGAAAGCTAATAATAACCATGCAAGGGATGATGACTAAAATGTTCTTAATAATCAAGATTTCTATTCTAATATAGAAACATAT

TTTTATAATGTTTATATGTTAGAACATACAACCCCACACCAAACACACCCAACACAA

5、GGTGTGGTTGGTTCACAGCTATTAAATGATGTGTTCAAGATCATTCACTTTGTAAATATACTTGATTCCAAAATCAAGAGAACCTATGCCTTTAAACCAGAGCTTCTCAAACGTCTCCTTGAAAGCTTTCCATGTTGGAGAAGCACAGATGTCTATAGCTGAGGTTCTGCAGCTACAACCAAACACACCCAACACAA

6、TGTTGGTTTGTACTGATGAGGGAGCTGGAAAAAGAGAATTTAAGCCTGAAAAGTGTGGAGGGGGCTTTAATGAGGGAGAGGAGGTACAACCTCTCAATAGGAGGAAGAACTAGACGAGAGAATCTTACTTCTCTTGCGAGCTCACTTCTCATAGTCTCCTCAGGTTCTGAGAGGACTTAGGGTTGGGATCCAAAACAACCCAAACACACCCAACACAA

7、TTGGTTTTGGTTTTTTGGACATGAAGTCCTTGCCCACGCCTATGTCCTGAATGGTAATGCCTAGGTTTTCTTCTAGGGTTTTTGTGGTTTAATTAGATCCCATTTGTCAATTTTGGCTTTTGTTGCCATTGCTTTTGGTGTTTTGGACATGAAGTCCTTGCCCACACCCCCCAAACACACCCAACACAA

9、GGGGGGGCTTGGCAGGCAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAAATACAAAAATTAGCCAGGCATGGTGGCGCACGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGTTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCAGAGATTGCGCCATTGCACTCCAGCCTGGGTGACAGAGTGAAACTCCTTCTCAAAAAAAAAAAAAATTACAAAATATAAATGAAAGAAATCAGAGGAGATCCAAATAAATAGAGAGACATATCATGTTCATGGATTGGAAGACGACACGGTAAAAAGGAGTGGAGTGCAGTGGCTCATGCGTGTAATCCCAGCACTTTGGGAGGTCAAGGTGGGAGATGGCTTGAGGCCAGGAATTCAAGATCAGCCTGGGCAACATGGTGAAACCCTCTCTCTACCAAAAATACAAAAATTAGTCAGACGTGATGGTGTGCACCTATAGTCCCAACTAGTCAGGAGGCTGATGTAGGAGGATTGCTTGAGCCCAGGAGGAGATCAAGGCTGTAAGTGAGTTGTGATTGCACCAAACACACCCAACACAA

10、GGGGGGTGGGGTACCAAAGATCACCGGAGATAAGGATTTCAACCCAGCCTGAAAGTGATGGAGATACCCAATCTCAACTCCTCTGGACTCAATTAAGACATAGTGGTGGCGCGTGCTGGCTTCCCAGCTACTCGGGAGGCTGAGGGAGAGAATCGTTTGAACCTGGGAGGCAGAGGTTGCTCTGAGCTAAGATTGCGCCATTGCACTCCACCCTGTGTGACCGAATGAAACTCCTTCTCAAAAAAAAAAAAAATTACAAAATATAAATGAAAGAAATCACAGGAGATCCAAATAAATAGAGAGACATATCATGTTCATGGATTGGAAGACTACACGTTAAAAAGGAGTGGAGTGCAGTGGCTCATGCGTGTAATCCCAGCACTTTGGGAGGTCAAGGTGGGAGATGGCTTGAGGCCAGGAATTCAAGATCAGCCTGGGCAACATGGTGAAACCCTCTCTCTACCACAAATACAAAAATTAGTCAGACGTGATGGTGTGCACCTATAGTCCCAACTAGTCAGGAGGCTGATGTAGGAGGATTGCTTGAGCCCAGGAGGAGATCAAGGCTGTAAGTGAGTTGTGATTGC

ACCAAACACACCCAACACA

11、

GTTGGTTTGTAATGTGCCAATTAGTACATAATTTGAATTTAATTGCTCTTCCTGATCATAGAATAGAGTAGACGGCTAGGCTTGATAAGGTTAGTAAAAATAGGAGGCCTATTTTAAAATTAATTAGAGGGTCTGGTATAGGGATGGGGGTTCACAACACCCCCAAACACACCCAACACAA

12、

TGGTGTTGGTCATACCAGTTAAAACATGGGGGAGGCTGGGCGTGGTGTTTCATGCCTGTAATCCCAGGACTTTGAGAGGCCAAGATGGCCAGATCATTTGAGGCCAAGAGTTGGAGACCAGCCTGGCCAACATTGCAAAACCCTAAAAATACAAAAATTACTAAAAGTAAAAAATTAGCTGTGTGTTTGGTGTTGTTTGGCAGGATGGTCTCGATCTCCTGACCTCGTGATCTGCCCGCCTCAGCCTCCCAAAGTGCTTGGATTACAGGCATGAGCCACCATGTGTAGCCAGTACTTCTTTTTTTATGGCCAAATAATATTCCACTGTGTGGATATACCATACTTTATCCATTCATCATCATCAGGTAATGGATATGTTTTGATTCTCTGCCCTACTTTATTTTTGAGACAGAGTATCACTCTGTTGCCCAGATTGTACTACTGCAGCCTCCAAATCCTGGGTTCTCAGCCTCCTGAATAGTTGGGATTACAGATGTGAACCAACCAACCAAACACACCCAACACAA

13、

GTTGGTTTGTAATGTGCCAATTAGTACATAATTTGAATTTAATTGCTCTTCCTGATCATAGAATAGAGTAGACGGCTAGGCTTGATAAGGTTAGTAAAAATAGGAGGCCTATTTTAAAATTAATTAGAGGGTCTGGTATAGGGATGGGGGTTCACAACACCCCCAAACACACCCAACACAA

14、

TTGGTGTGTTCCAATTAGGAAAAACGGGGAAAAAAGAAAAAAATTGAAAACATTATCTTGGAGACCTGTAGCCAGAAAAATCAGAATTCAATCCAAACTGTAGAAAACCCAAACACACCCAACACAA

15、

TTTTTTTTTTTTTGTGAGACACAGACTCTCTTTTTGTCACCCAGGGTGGAGTACAGTGGCACAATCTCCGCTCAGTGCAACCTCCATGTGCCGGGCTCGTGCATGTGACGTGTCTCCCCCTCCAGAGTATGGGGGATTATCACCACCCCCCCCAAACACCCCCAACACATATCTCTAGAAGATCCCGGGGCACCGATCTCAAATTCAAAATCGTGGATATATGTGTTTCGTGTGAGAAAGTGTTATCCTCTCACTATTCCACACAATATAAGACCCAGAAGCATAAAGTGTAAACCGTGGGGTGCCTAAAGAGAGATCTAACTCACATTATGTGCGTTGCTCTCAGTGCCCTTTTTCCTCTCGAAAAACCTGGCGTGCCCTCTGCTTTAGAGAATCGCACAACGCGCGGAGAGAGGCGGTGTGCATAGTGGGCTCTCTTCCTCTTCCTCTCTCAGAGACTCTGTGCTCTCTCTCTTTCCTGTGCCGAGAGCGATATCATCTCTCTCAAGGGGGGATATAGGGATATCCACAAAATCGGGGTATAACACGAGAAAAACGTGAGAGCAAGGGGCCAACAAAGGCCCAAGACCCATAAAAACGCCGCTGCTCTCGCGTTTCTCTAGACGCTGCGCCCCTCAGAAGAATCTCACAAATATCGACTCTCGACTGAGATGTGGAGAAACCCCACAAGTATATAAATATACGACGTTTTCCCTGTGAAATCTCTCTCGTGCGCTCTCGTGTCCACACTGTGCCGTTCAGCATACACGTGCCCCTCTCTCTCTTTCGAAA

AGCGTGGCTCTCTCTCATATCTCACGCTGTATGTATCACAGCTCTGTATATCTCGCGCTCTAAACGCTGGTGTGTGTGCGCACCCCCCCGTTCCCCCAAACGCTGCGCCCTTCCGGAAAATAGCGTGAGAGTACACCGGGTGAGACACACTTATCCCTCTGGCAGCCACTGTGTACAGATAGAGAGCGGT

16、GGTTTGGGTTACTGTGTTCACTGTCGTATCCCAGTGCAAAGAACACAGAAGGCACTCAAGATATAGCTACTGAATGCATGAATGGTGTCTCACAACCCTGTGAGGCTGGCATTATTGACATCCCAGGTTACAGATGAGGAAACCAGGGCTCAAGGAGGTTAGGTGACTTGCCTAAGGCCTCACAGCCCTGGACACTCCCATCACACTGGCCTTCTGCTCCCCAAACACACCCAACACAA

17、TGGACACCGCCAAAGTCCGGCTGCAGGTAGAGGGCGAGGCGGGGATGGGGGTGCATCTCAGGGCAGAAAGGGGCACCTGTGGGGGACACCCCTTTGATTCAGGCTTTGGTTTAACCGCCGTTTCTCAGGTAGGTACAGCAGGTGGCCGCCTGAAACACCAGTTTGACGTTGTCGCGGAACTGGATGCATTAGGGTGGGAAGCTGGAACTTTTCCAGGGTTAACTGCAAAATCTCAAGGACCGCGGGGATATGAATTGACCATGATTATTGTCAGACTCCAAAAGTTAGGGGGCACCCAGTGTTCTCAGAGCAAAGACCGTCAGCCCCTCTGGAGCTGACCAGCCAAGCTCTGTCTCCTTCCATCTTTGATTCAATGGAGGGGAGGGGGGTGAATCTTCCCCTCTTGTACCGTTCTGTGAATTTATGGATCTGATGGATGGAATTTTATGAAGATCCGTCGGAAATCCGAAGATAAGGCGCGCAGTCGGATTTTGCTCAAGATTGTTCTAGGATGGGGCCTAATTTTGTAACTTACCTCCCGTGGATGAAGGAACTGTTTCTGATACCGGTAGATAATTTTGTAGCCAGATCCATCGAGCACGTAAACACCGGCTACCAAAAAACTTGATAGATAACAACTTGTTCTGGGGGTTAACGTGAACCGATCGTATATGGATAGAATTCGAAATATGTATAGATAATTGATACTTTGAATCTTCCACCATATCTGGGGATTTTCAAGAAGGAACAACCTTCTTACATCCTGTGCGTCAATCCAGGTCTTTCCATCACGACGTGATCTGGCTGTCTTTATAGCGAATGTTTAACGATACGCCCTATGCTTAGCCTGTCCTTGCGAAGTTAAGCAGTTTTAGACGAGAGATGATATTAGCAGGTTCCGAT

18、GTTTGGTGTGCTCCTTGAAATGTCTTCACCCCTACACCTTGCTTCTAAAGGTCCTATCCCTTCCCTGAAGCCTGCCTAATCTATTCTAGATAGAGCATCCTCACCCTCTCAAACATGTCTGAACACACACCCCCACCAAACCCACCCTACACAA

19、TGGTGTGTTGAGCTGTGCCATTGAAAGAGTCTTGAACTCAGGCCGGCCTGGAGGTGGAGGTGGAGCTGTGCCAAACACACCCAACACAA

20、GGGGTGGTGGGGACCCAGGAAGGCCTGAGGTGAGCTATTTACCAGCCAGCGAAGGACTACACTTGACCCTAGAAGGACAGGGGTTTGAATCGTGTGGTCCACTTATATGTGGAC

21

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22
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23、
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24 、
TGTTGGTTTGTACTGATGAGGGAGCTGGAAAAAGAGAATTTAAGCCTGAAAAGTGTGGAGGGGGCTTTAATGAGGGAGAGGAGGTACAACCTCTCAA
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CAACCCAAACACACCCAACACAA

25 、
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26

GTTGGGGTTTTTGAAGCTGTTGACCTTTAGATGGGGTTTTTGTGGGGACTTTTTTGTTGATGTTTTTGTTGTTGCTTGCTGTTGCATTCCCCTTGCCCTGT
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CAAACCAAACACACCCAACACAA

27

GTTGGGGGGGACTACCAAATGATTCACCCCTACACCTGGCTGGAGACTTTCTTGATCTTGTTTTTGTTGTGCCTTGCTGCTGCTTTATCCAGCAGATTCA
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28、

GTGGTGGGGACCCAGGAAGGGCTGAGGTGAGCTATTTACCAGCCAGCGGAGGACTACACTTGACCCTTGTAGGACAGGGGTTTGAATAGTGGGGTCA
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29、

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30、

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31、

TGTGTGTGCATGTGTCTTTATAGCAGCATGATTTATAATCCTTTGGGTATATACCTAGTAATGGGATGGCTGGGTCAAACGGTATTTCTAGTTCTAGATCCTTGAGGAATCGCCACACTGACTTCCACAATGGTTGAACTAGTTTACAGTCCCAAAAACAAACCAAACACACCCAACACAA

32、

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33、

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34、

TTTTGTTTTTTCACTGGTCAGAACCAGTGTTGGTAGTAAGAATTATTGTCCCAGAAGAGAATGGAAATGCTTGCCAACTCTACTTTCAACCCTTGCTGGAATCCCTATGTTGTGGGTAGAGATATGACTAAATTAAGCAGTTTTAAGTCTAGGACACCAAACCCCAAACACACCCAACACAA

35、GGTAAAGGTGTGTCATGATGGTTTGCGGCACAGATCATCCTATCACCCAGTTATTAAGTCCAGTATTCATTAGTTTTTCTTTCTGATACTCTCTCTCCCCCACAACCAAACACACCCAACACAA

36、TGGTGGTTGTACTAAAAATAAGATGGGGTAGCAGGTGCTACATTTACTACCCTTTCTGAAACAACCAAACTGGCTGAAATATATAAAATACTTTTCAAGGTACTGGAACTTAGGTGATGTCTTAGTGCATTCAGGCTGCTATAACAAAACAAACCAAACACACCCAACACAA

37、GTGTGGGTTGACACGAAAGGTAACAAGACCATCCGTGCGGACTGGCGCACGCCGTTTCGGCATTTTTCAACGTGGCATATGCCGGAAGCTACGCACACGCGCGGGATGCGAGATTGGGCGCTATTTGACGCAGCCACAAACGGCGGGACGACCTGCCCTGCGACAATCAGCTATCAAAAGGACGCGGGCGCTAGCGGGTTTTTCCGGGTGCTAGCGTATAACCGCACCAAACACACCCAACACAA

38、GGGGGGGGTGACACGAACCGTAAAAGACCATCCGCGCGGACTGGCGCCCGCCACCTCGGTTTTTTCAACGGGGTTTATGCAGGAAGCTACCTACACTCGCGGGATGCGAGATTGGGCGCTATTTGACGCAGCCACAAACAGAAGGACGACCTGCCCTGCGACAATCAGCTATCAAAAGGACGCGGGCGCTAGCGGGTTTTTCCGGGTGCTAGCGTATAACCGCACCAAACACACCCAACACAA

39、GTTTTGTTTGGTAAAGGTGTGTCATGATGGTTTGCGGCACAGATCATCCTATCACCCAGTTATTAAGTCCAGTATTCATTAGTTTTTCTTTCTGATACTCTCTCTCCCCCACAACCAAACACACCCAACACAA

40、TGTTTGAGCATGTCCTTAGACACATGTTCAGATATGCTTCGTTATTCCCTTTAAGCCTTTTCTTTACTTTCTCCTTCACTTTTGTTACTCTCAATGCTAATGAATAATTGACCTCTTCGCCACAAAAAACCAAACACACCCAACACAA

41、TTTGGTTGCGGGTGCCTGCTACCCAGCTAGCTACCCAGTAGCGTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGACATGAACCCGGGAGGCGGAGCTTGGAGTGAGCCGAGATCGTGCCACTGCACTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAGAAAAAAGAAACTGTTATTAACAGCTCTATACCAACAAATTGGATAACCTAGAGTAAATGGATAAATTCTTAGAAACAACCAACCAAACACACCCAACACAA

42、TTTTTTTTCCTGTAAGGCTACACAGAAGAATTCTCAGTAACTTCCTTGTGTTGTGTGTATTCAACTCACAGAGTTGAACGATCCTTTACACAGAGCAGA

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43、

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44、

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45、

GTTTTGGTGGGGCGTGTAGAAGTCCACCAGCTGTTGAAGATGAGGCCAGGCGTCCTCAGAGGAGAGAACAGAAAGTGCCAAGGCCAGGGGCAGCGGTAAGGAGCACACGGCACACTGGGGAAGAGTCAAATGCTGGAGCCCAGGGTGTGGGCGGAGCGGTGGGAGATGAGGACACCCCGATGGCTTGGGGTCAGGTTCTGAAGAATGTTGGGTACTAGGCTCGAGTTTGGACTCTATGGTGGGGGAAATAGAGAGCCCCTGACAGTCTTTAAAGAGGGGAGAGATGGATCAGGCCTGTAGCATTTCCTCAGGGAGGTTATAAAGCAGGTACAGAGGTACAGACACATCTTCTGTGCTTATTTATGTCATGGGGCCTTTGCACATAGTTGGAGCCATGATTTACATAGCTGTGCTTCCCCATACCACCACACCAAACACACCCAACACAA

46、

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47、

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48、

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49、

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50、

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51、

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52、GTTTTTTGGTTTATATATAGAGATTCAAGTAATACTATTTTGAGAGTAATTTCTCTACATGAGTGGCTTTATCTCCATTCCGTCCTCATGGGAGTAGAAGACAAGTAAAAAGAAGATTCACACCCGCTGATTGATACGCCATGTCCTTTAGCTTTAGGTTTTTCCCCCTCCGTCCAAATTTTTACCAAAGCAGTGTTTAGTTGTCTGATTGAGTTTTATATCTTTTCTTTTTTCTAATTTATCCAATGAACATGCCAATAAAAACTGCCAAACACACCCAACACA

53、GTTTTGTTGTCATAAAATTTAACTTCATTTTAATCAAGGTGACAGGTAAATTCTTAAAATACCACCCAAACACCCCAAAAATCTCAGGCTTTCGCAGTCCTAAATAATGAGCATTATTAACTGTGTATTGTCTAGTCTAGACTTTGTGTGAAATTGTTACTCTGAATTTTAAATTGCTGTATACATTATTATATCTTGAGTAGTAATTCCTGCGGTGCCTAATATTAGATCTAGTATAATTGAATTTTACAAACTCTTATGTTAAAAACACTTTTCATTAACTGACATGTCCGACACAATCAAACACACCCAAAACAC

54、GGTTTAGGGTTATACATTTGAGAGACAGAAGAAAGCAAACTACTTCTTAACAAAATTGAACCTGTAACTTTGACCTAGTAGTCTCAGGCTTTCACTGAACTAAATGAGGCAGATTATAAACTGTGTATTGTTTAGTGGAGACTTTATGTTCTGTTAATACTCTGAATTTTAAATTGTTGTATAGATTATTATATCTAGTGTACAAATTAATACCAAATTCCGTATTAATTCAAGTATAATTGTACTTTACAAACTCTTAGCTTAAAAACAGTTTTCATTATGTGACATGTCAGAAACAACCAAACACACCCAACACAA

55、GCAGTGCCAGCTTGCATGCCTGCAGGTCGACGATTTGTGTTGGGTGTGTTTGGTGGACACCGCCAAAGTCCGGCTGCAGGTAGAGGGCGAGGCGGGGATGGGGGTGCATCTCAGGGCAGAAAGGGGCACCTGTGGGGGACACCCCTTTGATTCAGGCTTTGGTTTAACCGCCGTTTCTCAGGTAGGTACAGCAGGTGGCCGCCTGAAACACCAGTTTGACGTTGTCGCGGAACTGGATGCATTAGGGTGGGAAGCTGGAACTTTTCCAGGGTTAACTGCAAAATCTCAAGGACCGCGGGGATATGAATTGACCATGATTATTGTCAGACTCCAAAAGTTAGGGGGCACCCAGTGTTCTCAGAGCAAAGACCGTCAGCCCCTCTGGAGCTGACCAGCCAAGCTCTGTCTCCTTCCATCTTTGATTCAATGGAGGGGAGGGGGGTGAATCTTCCCCTCTTGTACCGTTCTGTGAATTTATGGATCTGATGGATGGAATTTTATGAAGATCCCGTCGGAAATCCGAAGATAAGGCGCGCAGTCGGATTTTGCTCAAGATTGTTCTAGGATGGGGCCTAATTTTGTAACTTACCTCCCGTGGATGAAGGAACTGTTTCTGATACCGGTAGATAATTTTGTAGCCAGATCCATCGAGCACGTAAACACCGGCTACCAAAAAACTTGATAGATAACAACTTGTTCTGGGGGTTAACGTGAACCGATCGTATATGGATAGAATTCGAAATATGTATAGATAATTGATACTTTGAATCTTCCACCATATCTGGGGATTTTCAAGAAGGAACAACCTTCTTACATCCTGTGCGTCAATCCAGGTCTTTCCATCACGACGTGATCTGGCTGTCTTTATAGCGAATGTTTAACGATACGCCCTATGCTTAGCCTGTCCTTGCGAAGTTAAGCAGTTTTAGACGAGAGATGATATTAGCAGGTTCCGAT

56

TGTGGGTGGTACACCTGAGGTCAGGAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACCAAAAATACAAAAATTAGCCGGATGTGGT
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57

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58

GGTTTAGGGTTATACATTTGAGAGACAGAAGAAAGCAAACTACTTCTTAACAAAATTGAACCTGTAACTTTGACCTAGTAGTCTCAGGCTTTCACTGAA
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ACACACCCAACACAAA

59

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60

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61

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62

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63

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64

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80

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81

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82

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92

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93

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94

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108

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112

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113

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114

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115

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116

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117

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118

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119

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120

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121

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122

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123

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124

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125

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126

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127

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128 号

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129

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130

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131

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132

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133

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134

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135

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136

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137

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138

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139

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140

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141

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142

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143

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144

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145

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146

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147
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148
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149
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150

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151

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152

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153

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154
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155
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156
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157
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158
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159
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160
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161
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162
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163
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164

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165

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166

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167

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168

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169

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170

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171

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172

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173

GGAGCCGAGGTGGGTGGATCACTTGAGGTCAGGAGTTTAAGACCAACCTAACCAACATGGCGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCC
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174

TGTTTTTGTGGTCCCTCACTTTCCTCCCCATTTGCATCTGTAGGGCACTTTATTTTAAATGCTGGATTCTTTTGCTCCAGAAAGTGGGAACTGGTGGGGA
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175

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176

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177

AGACTTCAGTTGCTCACTTTCAATAATGGATAGAAGATCTAGGTAAAAGATAACTAAGGAAATAGAGGATTGGAACAAAAACACCAAACACACCCAAC
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178

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179

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180

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181

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182

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183

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CGTT

184

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185

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186

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187

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188

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189

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190

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191

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192

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193

GGGGTTGTGTGTGTATGTGATTTTGTGTGTGCACTAATACACATGTAGGAGACCAAGGCAGGAGAATCACATATCCAAAGCCAAGCTGCCTACCAGGTT
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194

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